

GenCore version 5.1.6
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

:OM nucleic - nucleic search, using Bw model

Run on: January 31, 2004, 04:07:32 ; Search time 7213 Seconds
(without alignments) ; 10997.333 Million Cell-updates/sec

Title: US-10-017-085a-205

Sequence: 1 cgcctccggcttcggaggt.....aaaaaaaaaaaaaaaa 1939

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2888711 seqs, 20454813386 residues

Word size : 10

Total number of hits satisfying chosen parameters: 2792712

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

Database : GenEmbl:*

1: gb:ba:*

2: gb:htg:*

3: gb:in:*

4: gb:om:*

5: gb:ov:*

6: gb:pat:*

7: gb:Ph:*

8: gb:pl:*

9: gb:pr:*

10: gb:ro:*

11: gb:sts:*

12: gb:sy:*

13: gb:un:*

14: gb:vi:*

15: em:ba:*

16: em:fun:*

17: em:hum:*

18: em:in:*

19: em:mu:*

20: em:om:*

21: em:or:*

22: em:ov:*

23: em:pat:*

24: em:ph:*

25: em:pl:*

26: em:ro:*

27: em:sts:*

28: em:un:*

29: em:vi:*

30: em:htg:hum:*

31: em:htg:inv:*

32: em:htg:other:*

33: em:htg:mus:*

34: em:htg:pln:*

35: em:htg:rod:*

36: em:htg:mam:*

37: em:htg:vrt:*

38: em:by:*

39: em:htg:hum:*

40: em:htg:mus:*

41: em:htg:other:*

SUMMARIES

Result No. Score Query Match Length DB ID Description

Result No.	Score	Query	Match	Length	DB ID	Description
1	1635	84.3	1964	9	BC015582	BC015582 Homo sapi
2	1497	77.2	1779	6	AX195174	AX195174 Sequence
3	1061	54.7	175020	9	AC024267	AC024267 Homo sapi
4	200	10.3	397	6	AX01778	AX01778 Sequence
5	52	2.7	103555	10	AL669840	AL669840 Mouse DNA
6	52	2.7	204628	2	AC048361	AC048361 Mus muscu
7	51	2.6	51	6	AK163165	AK163165 Sequence
8	42	2.2	245259	2	AC114124	AC114124 Rattus no
9	31	1.6	177877	2	AC133243	AC133243 Rattus no
10	27	1.4	413	4	AB054499	AB054499 Phytocer
11	27	1.4	561	11	GG3447	GG3447 SHGC-141356
12	27	1.4	616	8	LDA03162	AJ003162 Laminaria
13	27	1.4	905	9	BC017773	BC017773 Homo sapi
14	27	1.4	917	10	BC022657	BC022657 Mus muscu
15	27	1.4	963	9	BC027481	BC027481 Homo sapi
16	27	1.4	1062	8	AHSRNAME	X96466 A. hispanicu
17	27	1.4	1174	9	BC008472	BC008472 Homo sapi
18	27	1.4	1322	9	HSM00573	AL000072 Homo sapi
19	27	1.4	1433	9	HSU1813	U41813 Human Class
20	27	1.4	1433	11	GL19993	GL19993 SWSS700 Bri
21	27	1.4	1588	9	AK026173	AK026173 Homo sapi
22	27	1.4	1836	10	MUSM81	DI4849 Mus muscu
23	27	1.4	2061	9	BC000591	BC000591 Homo sapi
24	27	1.4	2363	10	BC0052006	BC0052006 Mus muscu
25	27	1.4	2793	3	AY05943	AY05943 Drosophil
26	27	1.4	2800	9	BC033596	BC033596 Homo sapi
27	27	1.4	5640	10	BC023754	BC023754 Mus muscu
28	27	1.4	35055	8	NCB16114	AL151011 Neurospor
29	27	1.4	4496	10	AL645975	AL645975 Mouse DNA
30	27	1.4	61226	9	AL139392	AL139392 Human DNA
31	27	1.4	77448	2	AC06956	AC06956 Homo sapi
32	27	1.4	86064	8	AB013395	AB013395 Arabidops
33	27	1.4	111998	9	AC011509	AC011509 Homo sapi
34	27	1.4	114532	9	AC015950	AC015950 Homo sapi
35	27	1.4	114546	2	AC000382	AC000382 Homo sapi
36	27	1.4	129332	9	AL90028	AL90028 Human DNA
37	27	1.4	133797	2	AC05740	AC05740 Sus scrof
38	27	1.4	141775	9	AC079949	AC079949 Homo sapi
39	27	1.4	149646	2	AL163536	AL163536 Homo sapi
40	27	1.4	158553	2	AC00937	AC00937 Homo sapi
41	27	1.4	158802	2	AC015589	AC015589 Homo sapi
42	27	1.4	159577	9	AC078955	AC078955 Homo sapi
43	27	1.4	164135	2	AC102228	AC102228 Mus muscu
44	27	1.4	166380	9	AC087237	AC087237 Homo sapi
45	27	1.4	166966	9	AC016970	AC016970 Homo sapi

ALIGNMENTS

QY	1634	GTCTGCTAGTAGTTAATACCCCATGTTAATGAGCGAAATTAGGCCTCCGAGCTA	1693	CCTAGCCCGTGGGGTGTAGCCCTAGGCTCAGGCTCCACTGGGGAGCTGCTGACTCAA	670
Db	1633	GTCTGCTAGTAGTTAATACCCCATGTTAATGAGCGAAATTAGGCCTCCGAGCTA	1692	CCTAGCCCGTGGGGTGTAGCCCTAGGCTCAGGCTCCACTGGGGAGCTGCTGACTCAA	521
QY	1694	AGGGACTCGCTAGGCTCTCACAGTGGTAGTGGAGGAGGAGGAGCTGAACTGAGG	1753	CGCTGGACGCCAGTGTGGCTGGCTGGCCAGGGAGCTGGGATATGTGACACTAG	730
Db	1693	AGGGACTCGCTAGGCTCTCACAGTGGTAGTGGAGGAGGAGCTGAACTGAGG	1752	CGCTGGACGCCAGTGTGGCTGGCTGGCCAGGGAGCTGGGATATGTGACACTAG	581
QY	1754	TCTGAGGCCAGGCGCACTCGCGTAGATGGCTGAGAGTGTGACTCGGGAGGCG	1813	CTGCTTAATGACTGTTGCCGAGCTGGGAGACCCCTTCGGGCGATGCGGTGG	790
Db	1753	TCTGAGGCCAGGCGCACTCGCGTAGATGGCTGAGAGTGTGACTCGGGAGGCG	1812	CTGCTTAATGACTGTTGCCGAGCTGGGAGACCCCTTCGGGCGATGCGGTGG	641
QY	1814	CTGGATGAGGCTGCCATGGGAGGAGCTCCGGCGATGGGGCTGGGGCTGGAGG	1873	TGCTGCGCCACTTTGCCCATTTGGCTGCTGGCTGGCTGGCTGGGGCTGGAGG	850
Db	1813	CTGGATGAGGCTGCCATGGGAGGAGCTCCGGCGATGGGGCTGGGGCTGGAGG	1872	TGCTGCGCCACTTTGGCTGCTGGCTGGCTGGCTGGGGCTGGAGG	701
QY	1874	GTCATGTTCTGAGGCCCCCTGGATAAGCGGTGACGCCA	1933	GGCGACACCCCTGTTGGCTGCTGGCTGGCTGGGGCTGGGGCTGGAGG	910
Db	1873	GTCATGTTCTGAGGCCCCCTGGATAAGCGGTGACGCCA	1932	GGCGACACCCCTGTTGGCTGCTGGCTGGCTGGGGCTGGAGG	761
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AX195174		AX195174 Sequence 27 from Patent WO0151638.	1779 bp	DNA linear	PAT 28-AUG-2001
DEFINITION		ACCESSION AX195174		QY	
LOCUS		VERSION 4.1		Db	
AUTHORS		JI:15385737		QY	
KEYWORDS				Db	
SOURCE				QY	
ORGANISM				Db	
REFERENCE	1	Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.		QY	
YANG, J., BAUGHN, M.R., BURFORD, N., AU-YOUNG, J., LU, D.A., REDDY, R.,				Db	
RING, H.Z., HILLMAN, J.L., YUE, H., AZIMAI, Y., YAO, M.G., GANDHI, A.R.,				QY	
NGUYEN, D.B., TANG, Y.T., LAL, P. and BANDMAN, O.				Db	
TITLE		Drug metabolizing enzymes		QY	
JOURNAL		Patent: WO 0151638-A 27-19-JUL-2001;		Db	
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	1.	1-779		Db	
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	/db_xref="taxon:9606"			QY	
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ORIGIN				QY	
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Best Local Similarity	99.9%	; Pred. No. 0;		QY	
Matches 1547; Conservative	0;	Mismatches 1; Indels 0; Gaps 0;		Db	
QY	371	CAGGAGAGTGGAAATAGGGCTCTTCTGGGCTGGACTTGGCGAGCTGCGCTG	430	1242 TGGCCCTGGAGACTTCTTCGGTGGAGGATATGGTGAATTCTCTGGAG	1301
Db	222	CAGGAGAGTGGAAATAGGGCTCTTCTGGGCTGGACTTGGCGAGCTGCGCTG	281	1451 ATGACAGTAACTCCAGGAGATGGGTGACTGACAGCTCTGGCTGGCTGG	1510
QY	431	GTGGCGGCTTGGCACTGGCTTCTGGCTGGAGGAGCTGGCTGGCTGGCTGG	550	1302 ATGACAGTAACTCCAGGAGATGGGTGACTGACAGCTCTGGCTGGCTGG	1361
Db	282	GTGGCGGCTTGGCACTGGCTTCTGGCTGGAGGAGCTGGCTGGCTGGCTGG	341	1511 TGGATGAGTATTCAGGCCACCTTATGGTCACTGCTGGAGGAGCTGGAGG	1570
QY	491	AATGGCGGTATCAGTGGCTGGCGAGCGCTGGCTGGCTGGCTGGCTGG	610	1362 TTGGATGAGTATTCAGGCCACCTTATGGTCACTGCTGGCTGGAGGAGCTGG	1421
Db	342	AATGGCGGTATCAGTGGCTGGCGAGCGCTGGCTGGCTGGCTGGCTGG	401	1571 AGGGAGTTGCACTGATGCACTGGCCAAATGGAGATTAGTAGTGAATGATCCTTG	1630
QY	551	AACCATATCCTCCCTCTCTGAGACATCTGCTGCTGGCTGGCTGGCTGG	610	1422 AGGGAGTTGCACTGATGCACTGGCCAAATGGAGATTAGTAGTGAATGATCCTTG	1481
Db	402	AACCATATCCTCCCTCTCTGAGACATCTGCTGCTGGCTGGCTGGCTGG	461	1631 ACCCTCTAGTAGTTAATACCCCATGTTAATGAGGGATTAGCTCCGG	1690
QY				1482 ACCCTCTAGTAGTTAATACCCCATGTTAATGAGGGATTAGCTCCGG	1541

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repeat_region	8832..9133						
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repeat_region	9143..9415						
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repeat_region	10270..10279						
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repeat_region	10591..10872						
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repeat_region	10873..10886						
repeat_region	/rpt_ family=" (TAA)n"						
repeat_region	11232..11395						
repeat_region	/rpt_ family="FRAM"						
repeat_region	11395..11711						
repeat_region	/rpt_ family="ALUY"						
repeat_region	11712..11728						
repeat_region	/rpt_ family="FRAM"						
repeat_region	12424..12558						
repeat_region	/rpt_ family="LIM4"						
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repeat_region	/rpt_ family="ALUSX"						
repeat_region	15191..15223						
repeat_region	/rpt_ family="ALUSC"						
repeat_region	complement(145224..14691)						
repeat_region	/rpt_ family="MIR"						
repeat_region	14827..15139						
repeat_region	/rpt_ family="ALUSX"						
repeat_region	15788..15981						
repeat_region	/rpt_ family="ALUSG/x"						
repeat_region	complement(15983..16040)						
repeat_region	/rpt_ family="LIMCA"						
repeat_region	16055..16220						
repeat_region	/rpt_ family="ALUSG"						
repeat_region	16330..16510						
repeat_region	/rpt_ family="L2"						
repeat_region	complement(16512..16745)						
repeat_region	16746..17024						
repeat_region	/rpt_ family="ALUJ"						
repeat_region	complement(17025..17325)						
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 Db 91023 GCCCCATGGGAGTAAAGGGGAGCCCTCCGGCGATGCGGGGGATCTGTACT 90964
 COMMENT

TITLE	JOURNAL	Submitted	14-APR-2000	Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE	AUTHORS	3 (bases 1 to 204628)		
	Birren, B., Nusbaum, C., Lander, E., Abouelhail, A., Allen, N., Anderson, S., Arachchi, H.M., Barna, N., Batiashvili, V., Bloom, T., Boguslavsky, L., Bouthigalter, B., Camarati, J., Chang, J., Cheepel, Y., Collimore, A., Cook, A., Cooke, J., Corum, J., Dearlano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, J., Drickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardna, S., Graham, L., Grand-Pierre, N., Hafez, N., Higo, T., Higginson, D., Higginson, D., Higginson, D., Higgins, B., Hall, J., Horton, L., Huime, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Keils, C., Lenders, T., Levine, R., Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrum, J., Meneus, L., Mihowa, T., Mlengfu, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunikhong, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Rettar, R., Riese, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seainan, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Teufay, S., Theodore, J., Topham, K., Travers, M., Vassilie, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, I., Zimmer, A., and Zody, M.			
TITLE	JOURNAL	Submitted	12-MAR-2003	Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT		On Mar 27, 2003 this sequence version replaced gi:8076973.		
		All repeats were identified using RepeatMasker: http://ftp.genome.washington.edu/RM/RepeatMasker.html		
		Center: Whitehead Institute / MIT Center for Genome Research		
		Center code: WIBR		
		Web site: http://www-seq.wi.mit.edu		
		Contact: sequence_submissions@genome.wi.mit.edu		
		----- project Information.		
		Center project name: L7284		
		Center clone name: 163_A_8		
		----- Summary Statistics		
		Sequencing vector: M13, M7815, 33% of reads		
		Sequencing chemistry: plasmid, m13, 67% of reads		
		Chemistry: Dye-terminator		
		Big Dye: 10% of reads		
		Assembly program: Phrap, version 0.960731		
		Consensus quality: 20275 bases at least 040		
		Consensus quality: 203217 bases at least 030		
		Consensus quality: 203451 bases at least 020		
		Insert size: 197000, agarose-fp		
		Insert size: 203928, sum-of-contigs		
		Quality coverage: 12.1 in Q20 bases, agarose-fp		
		Quality coverage: 11.3 in Q20.		
		----- NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.		
		1 8112: contig of 8112 bp in length		
		8113 8122: gap of 100 bp		
		8113 9010: contig of 8897 bp in length		
		9010 9020: gap of 100 bp		
		----- FEATURES		
		source		
		----- ORIGIN		
		BASE COUNT 54328 a 49238 c 4710 g 53947 t 705 others		
		RESULT 7		
		AX163165 LOCUS AX163165		
		DEFINITION Sequence 6493 from Patent WO0140521.		
		ACCESSION AX163165		
		VERSION AX163165.1		
		KEYWORDS		
		SOURCE Homo sapiens (human)		
		ORGANISM Homo sapiens		
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Sutheria; Primates; Catarrhini; Hominidae; Homo.		
		REFERENCE 1		
		AUTHORS Shinketsu, R.A. and Leach, M.		
		TITLE Shinketsu, R.A. and Leach, M.		
		JOURNAL Nucleic acids containing single nucleotide polymorphisms and methods of use thereof		
		FEATURES Patent: WO 0140521-A 6493 07-JUN-2001, Curagen Corporation (US)		
		Source Location/Qualifiers		
		1..51 /organism="Homo sapiens"		
		/mol_type="genomic DNA"		

Query Match

Stanford Human Genome Center
 Stanford University School of Medicine
 4005 Miranda Ave. 2nd Fl., Palo Alto, CA 94025, USA
 Tel: (650) 320-5800
 Fax: (650) 320-5801
 Email: olivierobsgc.stanford.edu
 Primer A: ATTCAGAGGTGATGAGAGG
 Primer B: TGTCCACCGAGCTGAGACAGA
 SITS Size: 346

PCR Profile:

Initial incubation: 95 degrees C for 10 minutes
 Denaturation: 94 degrees C for 30 seconds
 Annealing: 60 degrees C for 30 seconds
 Polymerization: 72 degrees C for 23 seconds

Protocol:
 Thermal Cycler: Perkin Elmer: 9700
 Template: 25 ng
 each 1.0 μM
 dNTPs: each 1.00 μM
 AmpliQng Gold Polymerase: 0.07 units/μl
 Total Vol: 5 μl

Buffer:

MgCl2: 2.5 mM
 KCl: 50 mM
 Tris-HCl: 10 mM
 pH: 8.3

Finished human sequence in NCBI. STSs designed and developed at the
 Stanford Human Genome Center.
 Location/Qualifiers

1. .561

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 /db_xref="taxon:9606"
 /clone_id="bq-158"

/mol_type="genomic DNA"
 /db_xref="taxon:80365"
 /organism="Laminaria digitata"

STS
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 primer_bind
 complement (531. .553)
 BASE COUNT 176 a 161 c 133 g 151 t
 ORIGIN

Query Match 1.4%; Score 27; DB 11; Length 561;
 Best Local Similarity 100.0%; Pred. No. 0.0067;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 491 ACCGCCAAAGAAAGAAAGAAAGAA 517

RESULT 12
 IDA03162/c
 DEFINITION LDA03162 616 bp DNA linear PLN 12-JAN-2001
 ACCESSION AW003162
 VERSION AW003162.1
 SOURCE GR:3392938
 ORGANISM Laminaria digitata

Laminaria, stramenopiles; Phaeophyceae; laminariales; Laminariaceae; Laminaria.

REFERENCE Biller, C., Rousvoal, S., Estoup, A., Epplen, J.T., Saumitou-Laprade, P., Valero, M., and Kloeting, B. Isolation and characterization of microsatellite markers in the nuclear genome of the brown alga *Laminaria digitata* (Phaeophyceae). Mol. Ecol. 7 (12), 1778-1780 (1998)

REFERENCE MEDLINE 99076304
 PUBLISHED 9859207
 REFERENCE 2 (bases 1 to 616)

AUTHORS Billot, C.
 TITLE Direct Submission
 JOURNAL Submitted (27-Nov-1997) Billot C. Biologie Cellulaire et Moléculaire des Algues, Station Biologique CNRS, Place Georges Teissier, Roscoff, F-29682, FRANCE
 COMMENT uncoding region.
 FEATURES location/Qualifiers
 . source

BASE COUNT 167 a 134 c 143 g 172 t
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 Db 590 ACCGCCAAAGAAAGAA 564

RESULT 13
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 LOCUS BC017773 Homo sapiens, triggering receptor expressed on myeloid cells 1, clone MGC:22242 IMAGE:4692680, mRNA, complete cds.

ACCESSION BC017773
 VERSION BC017773.1
 KEYWORDS G1:1789458
 MGC.

SOURCE Homo sapiens (human)

ORGANISM Burkitt, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (bases 1 to 905)

REFERENCE 1 STRAUBERG, R.
 AUTHORS TITLE Direct Submission
 JOURNAL Submitted (03-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 COMMENT Contact: MGC Help desk
 Email: cpabs@rmal.nih.gov

Tissue Procurement: CLONTECH
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 cDNA Library Arrayed by: The T.M.A.G.B. Consortium (TLM)
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www-abgc.stanford.edu>
 Contact: (DICKSON, Mark) mdc@paxil.stanford.edu
 DICKSON, M., SCHMUTZ, J., GRIMWOOD, J., RODRIGUEZ, A., and MYERS, R. M.

Clone distribution: MGC clone distribution information can be found through the T.M.A.G.B. Consortium LINT at: <http://image.lnl.gov>
 Series: IRAL Plate: 36 Row: m Column: 14
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 8924261.
 Location/Qualifiers
 FEATURES source

/organism="Homo sapiens"
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 /lab_host="DHIOB"
 /note="Vector: pdnr-lib"
 46. .750

CDS

product="triggering receptor expressed on myeloid cells 1"	Query Match 1.4%; Score 27; DB 9; Length 905; Best Local Similarity 100.0%; Pred. No. 0.0065; Mismatches 0; Indels 0; Gaps 0; Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Db 870 ACGCCAANAAAANAAAANAAA 896
ORIGIN	Query Match 1.4%; Score 27; DB 9; Length 905; Best Local Similarity 100.0%; Pred. No. 0.0065; Mismatches 0; Indels 0; Gaps 0; Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Db 870 ACGCCAANAAAANAAAANAAA 896
BASE COUNT	258 a 224 c 224 g 199 t
RESULT 14	Query Match 1.4%; Score 27; DB 9; Length 905; Best Local Similarity 100.0%; Pred. No. 0.0065; Mismatches 0; Indels 0; Gaps 0; Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Db 870 ACGCCAANAAAANAAAANAAA 896
LOCUS	BC022657
DEFINITION	Mus musculus hypothetical protein LOC225847, mRNA (cDNA clone IMAGE:4219507), partial cds.
REFERENCE	1913 ACGCCAANAAAANAAAANAAA 1939
AUTHORS	Klausner, R.D., Collins, P.S., Wagner, L., Schreiner, C.M., Schuler, G.D., Attuchui, S.P., Zeeberg, B., Buetow, K.H., Schaefer, C.P., Bhat, N.K., Hopkins, R.P., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, P., Bratchenko, L., Macusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stippleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Uedin, T.B., Toshiyuki, S., Carninc, P., Pranke, C., Rana, S.S., Loqueland, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McElwan, P.J., McFernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muniz, D.M., Sodergren, B.J., Lu, X., Gibbs, R.A., Farley, J., Heitton, B., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Slepchenko, V., Boulard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D., Butterfield, V.S., Krzywinski, M.I., Skalski, U., Smalius, D.E., Schermer, A., Schein, J.B., Jones, S.J. and Maura, M.A.
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16099-16093 (2002)
MEDLINE	22388257
PUBMED	12477932
REFERENCE	(bases 1 to 917)
AUTHORS	Strausberg, R.
TITLE	Direct Submission
JOURNAL	Submitted (01-FEB-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgabs@mail.nih.gov Tissue Procurement: Jeffrey E. Green, M.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LNU) DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
COMMENT	
FEATURES	Source
ORIGIN	gene
LOCUS	BC022657
DEFINITION	Mus musculus hypothetical protein LOC225847, mRNA (cDNA clone IMAGE:4219507), partial cds.
REFERENCE	1913 ACGCCAANAAAANAAA 1939
AUTHORS	Klausner, R.D., Collins, P.S., Wagner, L., Schreiner, C.M., Schuler, G.D., Attuchui, S.P., Zeeberg, B., Buetow, K.H., Schaefer, C.P., Bhat, N.K., Hopkins, R.P., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, P., Bratchenko, L., Macusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stippleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Uedin, T.B., Toshiyuki, S., Carninc, P., Pranke, C., Rana, S.S., Loqueland, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McElwan, P.J., McFernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muniz, D.M., Sodergren, B.J., Lu, X., Gibbs, R.A., Farley, J., Heitton, B., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Slepchenko, V., Boulard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D., Butterfield, V.S., Krzywinski, M.I., Skalski, U., Smalius, D.E., Schermer, A., Schein, J.B., Jones, S.J. and Maura, M.A.
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16099-16093 (2002)
MEDLINE	22388257
PUBMED	12477932
REFERENCE	(bases 1 to 917)
AUTHORS	Strausberg, R.
TITLE	Direct Submission
JOURNAL	Submitted (01-FEB-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgabs@mail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LNU) DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
COMMENT	
FEATURES	Source
ORIGIN	gene
LOCUS	BC022657
DEFINITION	Mus musculus hypothetical protein LOC225847, mRNA (cDNA clone IMAGE:4219507), partial cds.
REFERENCE	1913 ACGCCAANAAAANAAA 1939
AUTHORS	Klausner, R.D., Collins, P.S., Wagner, L., Schreiner, C.M., Schuler, G.D., Attuchui, S.P., Zeeberg, B., Buetow, K.H., Schaefer, C.P., Bhat, N.K., Hopkins, R.P., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, P., Bratchenko, L., Macusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stippleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Uedin, T.B., Toshiyuki, S., Carninc, P., Pranke, C., Rana, S.S., Loqueland, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McElwan, P.J., McFernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muniz, D.M., Sodergren, B.J., Lu, X., Gibbs, R.A., Farley, J., Heitton, B., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Slepchenko, V., Boulard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D., Butterfield, V.S., Krzywinski, M.I., Skalski, U., Smalius, D.E., Schermer, A., Schein, J.B., Jones, S.J. and Maura, M.A.
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16099-16093 (2002)
MEDLINE	22388257
PUBMED	12477932
REFERENCE	(bases 1 to 917)
AUTHORS	Strausberg, R.
TITLE	Direct Submission
JOURNAL	Submitted (01-FEB-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgabs@mail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LNU) DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
COMMENT	

Center code: BCB-HGSC

Web site: <http://www.hgsc.bcm.tmc.edu/cana/>

Contact: amg@bcm.tmc.edu

Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M., Yoon, V.S., Kovis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M., Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL site: <http://image.lnl.gov>. This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.

FEATURES

Source

Location/Qualifiers

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 /lab_host="DRI10B"
 /note="vector: pCMV-SPORT6"

CDS

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 /protein_id="AAB27481.1"
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 DSAQD"
 BASE COUNT
 ORIGIN
 190 a 311 c 297 g 165 t

Query Match 1.4%; Score 27, DB 9; Length 963;
 Best Local Similarity 100%; Pred. No. 0.0065; Mismatches 0; Indels 0; Gaps 0;
 Matches 27; Conservative 0;
 QY 1913 ACCGCCAARAAARAAARAA 1939
 Db 920 ACCCCTTAAATTTTAAATTTA 946
 Search completed: January 31, 2004, 06:50:37
 Job time : 7223 secs

OM nucleic - nucleic search, using sw model
Run on: January 31, 2004, 04:39:02 / Search time 126 Seconds
(without alignments)
6792.396 Million cell updates/sec

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Perfect score: 1919
Sequence: 1 cggctcgccctcgaggt.....aaaaaaaaaaaaaaaaaaa 1939
Scoring table: Oligo-NTC
Gapop-60.0 , Gapext 60.0
Searched: 569978 seqs, 220691566 residues
Word size : 10

Total number of hits satisfying chosen parameters: 239297
Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

No.	Score	Query	Length	DB	ID	Description
1	26	1..3	1525	3	US-09-157-603-4	Sequence 4, Appl
2	26	1..3	1525	3	US-09-587-436-4	Sequence 4, Appl
3	26	1..3	1525	4	US-08-927-165A-4	Sequence 4, Appl
4	25	1..3	263	4	US-09-991-097-26	Sequence 26, Appl
5	24	1..3	38	4	US-09-325-545-7	Sequence 7, Appl
6	24	1..2	102	1	US-07-820-154A-10	Sequence 10, Appl
7	24	1..2	102	2	US-08-097-554A-10	Sequence 10, Appl
8	24	1..2	102	3	US-08-480-640A-10	Sequence 10, Appl
9	24	1..2	102	3	US-08-295-802-10	Sequence 10, Appl
10	24	1..2	102	3	US-08-686-968C-106	Sequence 106, Appl
11	24	1..2	102	3	US-08-488-237A-10	Sequence 10, Appl
12	24	1..2	102	4	US-08-3-75-992A-10	Sequence 10, Appl
13	24	1..2	102	4	US-08-472-679H-10	Sequence 10, Appl
14	24	1..2	102	5	PCT-US93-0324-10	Sequence 10, Appl
15	24	1..2	108	1	US-07-820-154A-32	Sequence 32, Appl
16	24	1..2	108	2	US-08-097-554A-32	Sequence 32, Appl
17	24	1..2	108	3	US-08-480-640A-32	Sequence 32, Appl
18	24	1..2	108	3	US-08-295-802-32	Sequence 32, Appl
19	24	1..2	108	3	US-08-488-237A-32	Sequence 32, Appl
20	24	1..2	108	4	US-08-3-75-992A-32	Sequence 32, Appl
21	24	1..2	108	4	US-08-472-679H-32	Sequence 32, Appl
22	24	1..2	108	5	PCT-US93-0324-32	Sequence 32, Appl
23	24	1..2	111	1	US-08-097-554A-78	Sequence 78, Appl
24	24	1..2	117	3	US-08-480-640A-78	Sequence 78, Appl
25	24	1..2	117	3	US-08-295-802-78	Sequence 78, Appl
26	24	1..2	117	3	US-08-686-968C-130	Sequence 130, Appl
27	24	1..2	117	3	US-08-686-968C-144	Sequence 144, Appl

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENT:

OM nucleic - nucleic search, using sw model
Run on: January 31, 2004, 04:39:02 / Search time 126 Seconds
(without alignments)
6792.396 Million cell updates/sec

Title: US-10-017-085A-205
Perfect score: 1919
Sequence: 1 cggctcgccctcgaggt.....aaaaaaaaaaaaaaaaaaa 1939
Scoring table: Oligo-NTC
Gapop-60.0 , Gapext 60.0
Searched: 569978 seqs, 220691566 residues
Word size : 10

Total number of hits satisfying chosen parameters: 239297
Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

No.	Score	Query	Length	DB	ID	Description
1	26	1..3	1525	3	US-09-157-603-4	Sequence 4, Appli
2	26	1..3	1525	3	US-09-587-436-4	Sequence 4, Appli
3	26	1..3	1525	4	US-08-927-165A-4	Sequence 4, Appli
4	25	1..3	263	4	US-09-991-097-26	Sequence 26, Appli
5	24	1..3	38	4	US-09-325-545-7	Sequence 7, Appli
6	24	1..2	102	1	US-07-820-154A-10	Sequence 10, Appli
7	24	1..2	102	2	US-08-097-554A-10	Sequence 10, Appli
8	24	1..2	102	3	US-08-480-640A-10	Sequence 10, Appli
9	24	1..2	102	3	US-08-295-802-10	Sequence 10, Appli
10	24	1..2	102	3	US-08-686-968C-106	Sequence 106, Appli
11	24	1..2	102	3	US-08-488-237A-10	Sequence 10, Appli
12	24	1..2	102	4	US-08-3-75-992A-10	Sequence 10, Appli
13	24	1..2	102	4	US-08-472-679H-10	Sequence 10, Appli
14	24	1..2	102	5	PCT-US93-0324-10	Sequence 10, Appli
15	24	1..2	108	1	US-07-820-154A-32	Sequence 32, Appli
16	24	1..2	108	2	US-08-097-554A-32	Sequence 32, Appli
17	24	1..2	108	3	US-08-480-640A-32	Sequence 32, Appli
18	24	1..2	108	3	US-08-295-802-32	Sequence 32, Appli
19	24	1..2	108	3	US-08-488-237A-32	Sequence 32, Appli
20	24	1..2	108	4	US-08-3-75-992A-32	Sequence 32, Appli
21	24	1..2	108	4	US-08-472-679H-32	Sequence 32, Appli
22	24	1..2	108	5	PCT-US93-00324-32	Sequence 32, Appli
23	24	1..2	111	1	US-08-097-554A-78	Sequence 78, Appli
24	24	1..2	117	3	US-08-480-640A-78	Sequence 78, Appli
25	24	1..2	117	3	US-08-295-802-78	Sequence 78, Appli
26	24	1..2	117	3	US-08-686-968C-130	Sequence 130, Appli
27	24	1..2	117	3	US-08-686-968C-144	Sequence 144, Appli

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ORGANISM: Mus Musculus
US-09-587-436-4

Query Match 1.3%; Score 26, DB 3; Length 1525;
Best Local Similarity 100.0%; Pred. No. 0.05; Mismatches 0; Indels 0; Gaps 0;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
GENERAL INFORMATION:
APPLICANT: KMLEC, ERIC B.
APPLICANT: RICE, MICHAEL C.
APPLICANT: SMITH, SHERYL T.
TITLE OF INVENTION: Mammalian and Human Rec2
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESS: KIMERAGEN, INC.
CITY: NEWTOWN
STATE: PA
COUNTRY: USA
ZIP: 18940
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ FOR WINDOWS VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/927,165A
FILING DATE: 4/35
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: HANSBURG, DANIEL
REGISTRATION NUMBER: 361565
REFERENCE/DOCKET NUMBER: 7991-010-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-504-4444
TELEFAX: 215-504-4545
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1525 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: CDNA
US-08-927-165A-4

RESULT 3
US-08-927-165A-4
Sequence 4, Application US/08927165A
Patent No. 6410226

GENERAL INFORMATION:
APPLICANT: TAKESAKO, KAZURO
APPLICANT: OKADO, TAKASHI
APPLICANT: YAGIHARA, TOMOKO
APPLICANT: KURADA, MASANOBU
APPLICANT: ONISHI, YOSHIMI
APPLICANT: KATO, IKUNOSHIN
APPLICANT: AKIYAMA, KAZUO
APPLICANT: YASUEDA, HIROSHI
APPLICANT: YAMAGUCHI, HIDEYO
TITLE OF INVENTION: ANTIGENIC PROTEIN ORIGINATING IN
TITLE OF INVENTION: MALASSERZIA
NUMBER OF SEQUENCES: 58

CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747

COMPUTER READABLE FORM:
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENT IN RELEASE #1.0, VERSION #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/091,097
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: WEINER, MARC S.
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 1422-0346P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 263
TYPE: NUCLEIC ACID
STRANDEDNESS: DOUBLE
TOPOLOGY: LINEAR
MOLECULE TYPE: CDNA TO mRNA

RESULT 5
US-09-325-554-7/C
Sequence 7, Application US/09325554
Patent No. 6410335
GENERAL INFORMATION:
APPLICANT: WEIDEL, KURT
APPLICANT: BRAND, JOACHIM
TITLE OF INVENTION: DNA DETECTION BY MEANS OF A STRAND REASSOCIATION COMPLEX
FILE REFERENCE: 0244200000
CURRENT APPLICATION NUMBER: US/09/325,554
CURRENT FILING DATE: 1999-06-04
PRIOR APPLICATION NUMBER: 198-24-900-4
PRIOR FILING DATE: 1998-06-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENT-IN VERSION 3.1
SEQ ID NO: 7
LENGTH: 38
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis

Query Match 1.3%; Score 26, DB 4; Length 1525;
Best Local Similarity 100.0%; Pred. No. 0.05; Mismatches 0; Indels 0; Gaps 0;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
GENERAL INFORMATION:
APPLICANT: WEIDEL, KURT
APPLICANT: BRAND, JOACHIM
TITLE OF INVENTION: DNA DETECTION BY MEANS OF A STRAND REASSOCIATION COMPLEX
FILE REFERENCE: 0244200000
CURRENT APPLICATION NUMBER: US/09/325,554
CURRENT FILING DATE: 1999-06-04
PRIOR APPLICATION NUMBER: 198-24-900-4
PRIOR FILING DATE: 1998-06-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENT-IN VERSION 3.1
SEQ ID NO: 7
LENGTH: 38
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis

RESULT 4
US-09-091-097-26
Sequence 26, Application US/09091097
Patent No. 6432407

FEATURE: /FEATURE:
 NAME/KEY: mibc signal
 LOCATION: (1). (1)
 OTHER INFORMATION: Phosphate linked to biotin via Aminolinker
 US-09-325-554-7

Query Match 1.2%; Score 24; DB 4; Length 38;
 Best Local Similarity 100.0%; Pred. 0.52%; Mismatches 0; Indels 0; Gaps 0;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1916 GCCAANAAAANAAAANAAA 1939
 Db 25 GCCAANAAAANAAAANAAA 2

RESULT 6 US-07-820-154A-10/c
 Sequence 10 Application US/07820154A
 Patent No. 5382425

GENERAL INFORMATION:
 APPLICANT: Cochran, Ph.D., Mark D
 TITLE OF INVENTION: Recombinant Swinepox Virus
 NUMBER OF SEQUENCES: 40
 CORRESPONDENCE ADDRESS:
 ADDRESS: John P. White
 STREET: 30 Rockefeller Plaza
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10112

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/820,154A
 FILING DATE: 19920113
 CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
 NAME: White, John P
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212)977-9550
 TELEFAX: 422523
 LENGTH: 102 base pairs

INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 102 base pairs

TYPE: NUCLIC ACID
 STRANDEDNESS: double
 TOPOLOGY: circular
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO

ORIGINAL SOURCE:
 ORGANISM: Plasmid
 IMMEDIATE SOURCE:
 CIRCLE: 520-17.5 (junction B)

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 OTHER INFORMATION: /product= "N-terminal peptide"
 OTHER INFORMATION: /number= 1
 OTHER INFORMATION: /standard_name= "Translation of synthetic DNA
 OTHER INFORMATION: sequence"
 FEATURES:
 NAME/KEY: CDS
 LOCATION: 100..102
 IDENTIFICATION METHOD: experimental
 OTHER INFORMATION: /partial

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 Best Local Similarity 100.0%; Pred. No. 0.47%; Mismatches 0; Indels 0; Gaps 0;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1916 GCCAANAAAANAAAANAAA 1939
 Db 78 GCCAANAAAANAAAANAAA 55

RESULT 7 US-08-097-554A-10/c
 Sequence 10 Application US/08097554A
 Patent No. 5869312

GENERAL INFORMATION:
 APPLICANT: Cochran, Ph.D., Mark D
 TITLE OF INVENTION: Recombinant Swinepox Virus
 NUMBER OF SEQUENCES: 112
 CORRESPONDENCE ADDRESS:
 ADDRESS: John P. White
 STREET: 30 Rockefeller Plaza
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10112

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/097,554A
 FILING DATE: JULY 22, 1993
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
 NAME: White, John P
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212)977-9550
 TELEFAX: 422523
 LENGTH: 102 base pairs

INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 102 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: circular
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Plasmid
 IMMEDIATE SOURCE:
 CIRCLE: 520-17.5 (junction B)

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 LOCATION: 85..99
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 OTHER INFORMATION: /products= "N-terminal peptide"
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 OTHER INFORMATION: /standard_name= "Translation of synthetic DNA sequence"
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 OTHER INFORMATION: /evidence= EXPERIMENTAL
 OTHER INFORMATION: /gene= "lacZ"
 OTHER INFORMATION: /number= 2
 OTHER INFORMATION: /standard_name= "Translation of synthetic DNA sequence"
 PUBLICATION INFORMATION:
 AUTHORS: Ferrari, Franco A
 AUTHORS: Trach, Kathleen
 AUTHORS: Hoch, James A
 TITLE: Sequence Analysis of the spoOB Locus Reveals
 TITLE: a Polycistronic Transcription Unit
 JOURNAL: J. Bacteriol.
 VOLUME: 161
 ISSUE: 2
 PAGES: 556-562
 DATE: Feb.-1985
 US-08-097-554A-10

Query Match 1.2%; Score 24; DB 2; Length 102;
 Best Local Similarity 100.0%; Pred. No. 0.47; 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1916 GCCAAGAAAGAAAGAAAGAAAGAA 1939
 Db 78 GGCAGAAAGAAAGAAAGAAAGAA 55

RESULT 8
 US-08-480-640A-10/C
 Sequence 10, Application US/08480640A
 ;
 GENERAL INFORMATION:
 APPLICANT: Cochran, Mark D.
 APPLICANT: Cochran, Mark D.
 TITLE OF INVENTION: Recombinant Swinepox Virus
 NUMBER OF SEQUENCES: 225
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: John P. White
 STREET: 1185 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/480,640A
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: White, John P
 REGISTRATION NUMBER: 28,678
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 278-0400

TELEFAX: (212) 391-0525
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 102 base Pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLLOGY: circular
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Plasmid
 IMMEDIATE SOURCE:
 CLONE: 520-17.5 (Junction B)

FEATURE:
 NAME/KEY: CDS
 LOCATION: 85..99
 IDENTIFICATION METHOD: experimental
 OTHER INFORMATION: /partial
 OTHER INFORMATION: /codon_start= 85
 OTHER INFORMATION: /functions= "Translational start of hybrid protein"
 OTHER INFORMATION: /product= "N-terminal peptide"
 OTHER INFORMATION: /numbers= 1
 OTHER INFORMATION: /standard_name= "Translation of synthetic DNA sequence"
 OTHER INFORMATION:
 NAME/KEY: CDS
 LOCATION: 100..102
 IDENTIFICATION METHOD: experimental
 OTHER INFORMATION: /partial
 OTHER INFORMATION: /codon_start= 100
 OTHER INFORMATION: /functions= "marker enzyme"
 OTHER INFORMATION: /product= "Beta-Galactosidase"
 OTHER INFORMATION: /evidence= EXPERIMENTAL
 OTHER INFORMATION: /gene= "lacZ"
 OTHER INFORMATION: /number= 2
 OTHER INFORMATION: /standard_name= "Translation of synthetic DNA sequence"
 PUBLICATION INFORMATION:
 AUTHORS: Ferrari, Franco A
 AUTHORS: Trach, Kathleen
 AUTHORS: Hoch, James A
 TITLE: Sequence Analysis of the spoOB Locus Reveals
 TITLE: a Polycistronic Transcription Unit
 JOURNAL: J. Bacteriol.
 VOLUME: 161
 ISSUE: 2
 PAGES: 556-562
 DATE: Feb.-1985
 US-08-480-640A-10

Query Match 1.2%; Score 24; DB 3; Length 102;
 Best Local Similarity 100.0%; Pred. No. 0.47; 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1916 GCCAAGAAAGAAAGAAAGAAAGAA 1939
 Db 78 GGCAGAAAGAAAGAAAGAAAGAA 55

RESULT 9
 US-08-295-802-10/C
 Sequence 10, Application US/08295802
 ;
 GENERAL INFORMATION:
 APPLICANT: Cochran, Ph.D., Mark D
 APPLICANT: Cochran, Ph.D., Mark D
 TITLE OF INVENTION: Recombinant Swinepox Virus
 NUMBER OF SEQUENCES: 188
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: John P. White
 STREET: 30 Rockefeller Plaza
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10112

COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/295,802
 FILING DATE: Herewith
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: White, John P
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 977-9550
 TELEFAX: (212) 664-0525
 TELEX: 422523
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 102 base pairs
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: circular
 MOLECULE TYPE: DNA (genomic)
 ORIGINAL SOURCE:
 ORGANISM: Plasmid
 IMMEDIATE SOURCE:
 CLONE: 520-17.5 (Junction B)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 85..99
 OTHER INFORMATION: /codon_start= 85;
 OTHER INFORMATION: /functions="translational start of hybrid protein"
 OTHER INFORMATION: /products="N-terminal peptide"
 OTHER INFORMATION: /number= 1
 OTHER INFORMATION: /standard_name= "translation of synthetic DNA"
 OTHER INFORMATION: /sequence"
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 100..102
 IDENTIFICATION METHOD: experimental
 OTHER INFORMATION: /partial
 OTHER INFORMATION: /codon_start= 100
 OTHER INFORMATION: /functions="marker enzyme"
 OTHER INFORMATION: /products="Beta-Galactosidase"
 OTHER INFORMATION: /genes="lacZ"
 OTHER INFORMATION: /number= 2
 OTHER INFORMATION: /citation= ([1])
 PUBLICATION INFORMATION:
 AUTHORS: Ferrari, Franco A
 AUTHORS: Trach, Kathleen
 AUTHORS: Hoch, James A
 TITLE: Sequence Analysis of the spo0B Locus Reveals
 TITLE: a Polycistronic Transcription Unit
 JOURNAL: J. Bacteriol.
 VOLUME: 161
 ISSUE: 2
 PAGES: 556-562
 DATE: Feb. 1985
 /US-08-295,802-10
 Query Match 1.2%; Score 24; DB 3; Length 102;
 Best Local Similarity 100.0%; Pred. No. 0.47; No. 0;
 Matches 24; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;
 /US-08-295,802-10
 Sequence 106, Application US/0866658C
 Patent No. 6221361
 GENERAL INFORMATION:
 APPLICANT: Cochran, Mark D.
 APPLICANT: Junker, David E.
 TITLE OF INVENTION: Recombinant Swinepox Virus
 FILE REFERENCE: 39119-H/001
 CURRENT APPLICATION NUMBER: US/08/686,968C
 CURRENT FILING DATE: 1996-07-25
 NUMBER OF SEQ ID NOS: 231
 SEQ ID NO: 106
 SEQ ID NO: 106
 LENGTH: 102
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Homology
 OTHER INFORMATION: vector 520-17.5
 US-08-686,968C-106
 Query Match 1.2%; Score 24; DB 3; Length 102;
 Best Local Similarity 100.0%; Pred. No. 0.47; No. 0;
 Matches 24; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;
 /US-08-686,968C-106
 Qy 1916 GCCAAGAAAGAAAGAAAGAAAGAA 1939
 Db 78 GCCAAGAAAGAAAGAAAGAAAGAA 55
 RESULT 11
 US-08-488-237A-10/C
 sequence 10, Application US/08488237A
 Patent No. 6251403
 GENERAL INFORMATION:
 APPLICANT: Cochran, Mark D.
 APPLICANT: Junker, David E.
 TITLE OF INVENTION: Recombinant Swinepox Virus
 NUMBER OF SEQUENCES: 225
 CORRESPONDENCE ADDRESS:
 ADDRESS: John P. White
 STREET: 1185 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/488,237A
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: White, John P
 REGISTRATION NUMBER: 28,678
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 278-0400
 TELEFAX: (212) 391-0525
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 102 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: circular
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Plasmid
 IMMEDIATE SOURCE:
 CLONE: 520-17.5 (Junction B)

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/472,679H

FILING DATE: 07-Jun-1995

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Salkeld, Pamela G.

REGISTRATION NUMBER: 38,607

TELECOMMUNICATION INFORMATION:

TELEPHONE: (908) 298-2135

TELEFAX: (908) 298-5388

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 102 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Plasmid

IMMEDIATE SOURCE:

CLONE: 520-17.5 (Junction B)

FEATURE:

NAME/KEY: CDS

LOCATION: 100..102

IDENTIFICATION METHOD: experimental

OTHER INFORMATION: /partial /codon_start= 100

/functions= "marker enzyme" /products= "Beta-Galactosidase"

/evidence= EXPERIMENTAL

/genes= "lacZ"

/number= 2

/citation= ([1])

PUBLICATION INFORMATION:

AUTHORS: Ferrari, Franco A; Trach, Kathleen; Hoch, James A

TITLE: Sequence Analysis of the spoOB Locus Reveals a

Patent No. 6,497,882

Polycistrionic Transcription Unit

JOURNAL: J. Bacteriol.

VOLUME: 161

ISSUE: 2

PAGES: 556-562

DATE: Feb. 1985

SEQUENCE DESCRIPTION: SEQ ID NO: 10:

US-08-472-679H-10

Query Match

Best Local Similarity

100.0%

Score 24;

DB 4;

Length 102;

Matches 24;

Conservative 0;

Mismatches 0;

Indels 0;

Gaps 0;

/

Qy

1916

GCCAAGAAAGAAAGAAAGAAAGAA

1939

/

Db

78

GCCAAGAAAGAAAGAAAGAAAGAA

55

/

RESULT 14

PCT-US93-00324-10/C

Sequence 10, Application PC/US9300324.

GENERAL INFORMATION

/

APPLICANT: Cochran, Ph. D., Mark D

/

APPLICANT: Junker, M.S., David B

TITLE OF INVENTION: Recombinant Swinepox Virus

NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:

ADDRESSEE: John P. White

STREET: 30 Rockefeller Plaza

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10112

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/00324

FILING DATE: 19930113

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: White, John P

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 977-9550

TELEFAX: (212) 664-0525

TELEX: 42253

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 102 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Plasmid

IMMEDIATE SOURCE:

CLONE: 520-17.5 (Junction B)

FEATURE:

NAME/KEY: CDS

LOCATION: 100..102

IDENTIFICATION METHOD: experimental

OTHER INFORMATION: /partial

/codon_start= 100

/functions= "marker enzyme"

/products= "N-terminal peptide"

/number= 1

/standard_name= "translation of synthetic DNA

SEQUENCE DESCRIPTION:

/citation= ([1])

PUBLICATION INFORMATION:

AUTHORS: Ferrari, Franco A

TITLE: Sequence Analysis of the spoOB Locus Reveals a

Patent No. 6,497,882

Polycistrionic Transcription Unit

JOURNAL: J. Bacteriol.

VOLUME: 161

ISSUE: 2

PAGES: 556-562

DATE: Feb. 1985

SEQUENCE DESCRIPTION: SEQ ID NO: 10:

US-08-472-679H-10

Query Match

Best Local Similarity

100.0%

Score 24;

DB 5;

Length 102;

Matches 24;

Conservative 0;

Mismatches 0;

Indels 0;

Gaps 0;

/

Qy

1916

GCCAAGAAAGAAAGAAAGAAAGAA

1939

/

Db

78

GCCAAGAAAGAAAGAAAGAAAGAA

55

/

Matches	24	Conservative	0	Mismatches	0	Indels	0	Gaps	0	Best Local Similarity	100.0%	Pred.	No.	0.47	Matches	24	Conservative	0	Mismatches	0	Indels	0	Gaps	0
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Db	78	GCCAAAGAAAGAAAGAAAGAA	55	Db	81	GCCAAAGAAAGAAAGAAAGAA	59																	
RESULT 15												Search completed: January 31, 2004, 08:03:22												
US-07-820-154A-32/C												Job time : 128 secs												
Sequence 32, Application US/07820154A																								
Patent No. 5,382,25																								
GENERAL INFORMATION:																								
APPLICANT: Cochran Ph.D., Mark D.																								
APPLICANT: Junker M.S., David E.																								
TITLE OF INVENTION: Recombinant Swinepox Virus																								
NUMBER OF SEQUENCES: 40																								
CORRESPONDENCE ADDRESS:																								
ADDRESSEES: John P. White																								
STREET: 30 Rockefeller Plaza																								
CITY: New York																								
STATE: New York																								
COUNTRY: USA																								
ZIP: 10112																								
COMPUTER READABLE FORM:																								
MEDIUM TYPE: Floppy disk																								
COMPUTER: IBM PC compatible																								
OPERATING SYSTEM: PC-DOS/MS-DOS																								
SOFTWARE: Patent in Release #1.0, Version #1.25																								
CURRENT APPLICATION DATA:																								
APPLICATION NUMBER: US/07/820,154A																								
FILING DATE: 19920113																								
CLASSIFICATION: 424																								
ATTORNEY/AGENT INFORMATION:																								
NAME: White, John P.																								
TELECOMMUNICATION INFORMATION:																								
TELEPHONE: (212)977-9550																								
TELEFAX: (212)664-0525																								
TELEX: 422523																								
INFORMATION OR SEQ ID NO: 32:																								
SEQUENCE CHARACTERISTICS:																								
LENGTH: 108 base pairs																								
STRANDEDNESS: double																								
TYPE: NUCLEAR Acid																								
TOPOLOGY: circular																								
MOLECULE TYPE: DNA (genomic)																								
HYPOTHETICAL: NO																								
ANTI-SENSE: NO																								
ORIGINAL SOURCE:																								
ORGANISM: Plasmid																								
IMMEDIATE SOURCE:																								
CLONE: 53B-46.26 (Junction B)																								
FEATURE:																								
NAME/KEY: exon																								
LOCATION: 88-102																								
OTHER INFORMATION: /codon_start= 88																								
OTHER INFORMATION: /function= "translational_start of hybrid protein"																								
OTHER INFORMATION: /product= "N-terminal peptide"																								
OTHER INFORMATION: /numbers= 1																								
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FEATURE:																								
NAME/KEY: CDS																								
LOCATION: 103-108																								
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Db	81	GCCAAAGAAAGAAAGAA	59	Db	81	GCCAAAGAAAGAAAGAA	59							

QY	541	GCCTCGGTGAAACCATATCGGCCCCCTTCTGAKATCTGCTGCTGCTGAA	600	OY
Db	541	GCCTCGGTGAAACCATATCGGCCCCCTTCTGAKATCTGCTGCTGCTGAA	600	Db
QY	601	GGCATTTGCCCTAGCCCGTGTGGTGTAGCTCACCTGCCACCTGGAGCT	660	QY
Db	601	GGCATTTGCCCTAGCCCGTGTGGTGTAGCTCACCTGCCACCTGGAGCT	660	Db
QY	661	TGACTCTAACCCCTGACCGCGTGTGGTGTAGCTCACCTGCCACCTGGAGCT	720	QY
Db	661	TGACTCTAACCCCTGACCGCGTGTGGTGTAGCTCACCTGCCACCTGGAGCT	720	Db
QY	661	TGACTCTAACCCCTGACCGCGTGTGGTGTAGCTCACCTGCCACCTGGAGCT	720	QY
Db	661	TGACTCTAACCCCTGACCGCGTGTGGTGTAGCTCACCTGCCACCTGGAGCT	720	Db
QY	721	TGACACTAAGCTGCTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGAA	780	OY
Db	721	TGACACTAAGCTGCTATGCTCTGCTGCTGCTGCTGCTGCTGCTGAA	780	Db
QY	781	TGCGTCACTGCTATGAGCCACCCAGGGCTGTGACTCGGAGATGCTGCGCA	840	QY
Db	781	TGCGTCACTGCTATGAGCCACCCAGGGCTGTGACTCGGAGATGCTGCGCA	840	Db
QY	841	TGTCCTCTGATGCTGCTGAGCCACCTTTCGCCATGCTGCTGCTGCTGCGCA	900	QY
Db	841	TGTCCTCTGATGCTGCTGAGCCACCTTTCGCCATGCTGCTGCTGCTGCGCA	900	Db
QY	901	AGAGGGGTGCCAGACCCCTGCTCAAGAGGGATGAGCCCTCAG	960	OY
Db	901	AGAGGGGTGCCAGACCCCTGCTCAAGAGGGATGAGCCCTCAG	960	Db
QY	961	TGGAGATATTTCGCACTGCATGCTGAGAGGCTCTCGAGCTCCGAGACCG	1020	QY
Db	961	TGGAGATATTTCGCACTGCATGCTGAGAGGCTCTCGAGCTCCGAGACCG	1020	Db
QY	1021	GCGAGCCATCGCTATGGAGCCACAGAGGCTGGCTGGCTGGAGGAGGA	1080	QY
Db	1021	GCGAGCCATCGCTATGGAGCCACAGAGGCTGGCTGGCTGGAGGAGGA	1080	Db
QY	1081	TCTGTGACCCGTAAGACCCCTGAGCTGAGACTCTAGAGGCCCTCTAACAC	1140	QY
Db	1081	TCTGTGACCCGTAAGACCCCTGAGCTGAGACTCTAGAGGCCCTCTAACAC	1140	Db
QY	1141	CCCCAACCTGAGGAGCCACGTTCTCACTTACCGCTTCAAGGTCTAACAGCA	1200	QY
Db	1141	CCCCAACCTGAGGAGCCACGTTCTCACTTACCGCTTCAAGGTCTAACAGCA	1200	Db
QY	1201	TTGTCTAAGATGAGCACCGAATTAGGTAAAGTGTGAGCTGATCCAGCTCTCA	1260	QY
Db	1201	TTGTCTAAGATGAGCACCGAATTAGGTAAAGTGTGAGCTGATCCAGCTCTCA	1260	Db
QY	1261	ACCTCTAGGCGCAGGAACTGCGATGCCACTCATGCTCTGAAACCTCGATG	1320	QY
Db	1261	ACCTCTAGGCGCAGGAACTGCGATGCCACTCATGCTCTGAAACCTCGATG	1320	Db
QY	1321	TGAGGCGCTGCGACACTGAGGGTTGAGATCTGACCTCCGGTACTCTCTG	1380	QY
Db	1321	TGAGGCGCTGCGACACTGAGGGTTGAGATCTGACCTCCGGTACTCTCTG	1380	Db
QY	1381	GGCCCAAGCTGCGCTGGACACTCTCTCTCTGTGAGGAATTATGGGTGATT	1440	QY
Db	1381	GGCCCAAGCTGCGCTGGACACTCTCTCTGTGAGGAATTATGGGTGATT	1440	Db
QY	1441	TCTCTCTGAGACTGACGTAACCCCACTGGAGAGGAGCTATGACCTGCT	1500	QY
Db	1441	TCTCTCTGAGACTGACGTAACCCCACTGGAGAGGAGCTATGACCTGCT	1500	Db
QY	1501	TCTCGGAAATTGGAGTAGTATTCTGGCCACACCTATGATCTGATCAGCTG	1560	QY
Db	1501	TCTCGGAAATTGGAGTAGTATTCTGGCCACACCTATGATCTGATCAGCTG	1560	Db
QY	1561	GACGAGGAGGAGGTTGAGTGTGAGCTGACCATGAAATTAGTAGTGA	1620	QY
Db	1561	GACGAGGAGGAGGTTGAGTGTGAGCTGACCATGAAATTAGTAGTGA	1620	Db
QY	1620	GACGAGGAGGAGGTTGAGTGTGAGCTGACCATGAAATTAGTAGTGA	1620	QY
QY	1620	GACGAGGAGGAGGTTGAGTGTGAGCTGACCATGAAATTAGTAGTGA	1620	QY
RESULT 2				
ID	AJX87266	standard; cDNA; 1939 bp.	XX	
XX	AJX87266;		AC	
XX	27-SEP-1999	(first entry)	DT	
XX	CDNA clone	encoding human PRO853, amplified in tumour cells.	DB	
XX	PRO853; UNQ419; tumour; cancer; diagnosis; therapy; human; ds	.	XX	
XX	OS		XX	
XX	Homo sapiens.		XX	
XX	Location/Qualifiers		XX	
XX	Key		XX	
XX	PT		XX	
XX	CDS		XX	
XX	128..1261		XX	
XX	/+tag= a		XX	
XX	SIG_peptide		XX	
XX	128..175		XX	
XX	/+tag= b		XX	
XX	176..1258		XX	
XX	nat_peptide		XX	
XX	/+tag= c		XX	
XX	PN		XX	
XX	W0993170-A2.		XX	
XX			XX	
XX	PD		XX	
XX	15-JUL-1999.		XX	
XX	PP		XX	
XX	05-JAN-1999;	99W0-US0106.	XX	
XX	PR		XX	
XX	20-NOV-1998;	98US-0109304.	XX	
PR	05-JAN-1998;	98US-0070440.	PR	
PR	29-APR-1998/	98US-0083500.	PR	
PR	22-MAY-1998/	98US-008644.	PR	
PR	10-JUN-1998/	98US-0088742.	PR	
PR	10-NOV-1998/	98US-0107783.	PR	
XX			XX	
PA	(GETH) GENENTECH INC.		PA	
XX			XX	
PI	Boettstein D, Goddard A, Gurney AL, Hillian KJ, Lawrence DA		PI	
PI	Roy MA, Wood WI;		PI	
XX			XX	
DR	WPI, 1999-430385/36.		DR	
DR	P-PSDB; AAY06489.		DR	
XX			XX	
PT	Antibody against proteins expressed in neoplastic cells, useful for		PT	
XX	tumor diagnosis and treatment		XX	
PS	Example 1; FIG 25A-B, 1620p; English.		PS	

Query	Match	Score	1939	DB	20	Length	1939
Matches	Beet	Local	Similarity	1939	1939	1939	1939
1939	Conservative	100.0%	Pred.	No.	0	Mismatches	0
Qy	1	CACCTCCCTTGGAGCTGAGCCGGGGGGCGTTAGGGCTGAGGGAT	60	1	CACCTCCCTTGGAGCTGAGCCGGGGGGCGTTAGGGCTGAGGGAT	60	1
Db	61	CGCGAGGGCTGGGGCGTGGGGCGTGGGGCGGGCGCGTTCAGGGAT	60	61	CGCGAGGGCTGGGGCGTGGGGCGGCGGGCGCGTTCAGGGAT	60	61
Qy	61	CGCGAGGGCTGGGGCGTGGGGCGGCGGGCGGGCGGGCGGGCG	120	61	CGCGAGGGCTGGGGCGGCGGGCGGGCGGGCGGGCGGGCG	120	61
Db	121	GGCGGCTATGGGGGGCGCTGTGGGGGGGGGGGGGGGGGGGGGGGG	120	121	GGCGGCTATGGGGGGCGCTGTGGGGGGGGGGGGGGGGGGGGGG	120	121
Qy	121	GGCGGCTATGGGGGGCGCTGTGGGGGGGGGGGGGGGGGGGGGG	180	121	GGCGGCTATGGGGGGCGCTGTGGGGGGGGGGGGGGGGGGGGGG	180	121
Db	181	CTRACTACACTCTGTGAGGCCCCCGCGCGCGCGCGCGCGCG	240	181	CTRACTACACTCTGTGAGGCCCCCGCGCGCGCGCGCGCG	240	181
Qy	301	CCGGGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	300	301	CCGGGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	300	301
Db	361	CGAACCTGGCCAGGAAGAGGAAATAGGGCTCTTGTGGCGCG	360	361	CGAACCTGGCCAGGAAGAGGAAATAGGGCTCTTGTGGCGCG	360	361
Qy	361	CGGGGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	360	361	CGGGGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	360	361
Db	421	TCTGGGCTGGGGGGCTTGGGGCTTGGGGCTTGGGGCTTGGGG	420	421	TCTGGGCTGGGGGGCTTGGGGCTTGGGGCTTGGGGCTTGGGG	420	421
Qy	421	TCTGGGCTGGGGGGCTTGGGGCTTGGGGCTTGGGGCTTGGGG	480	421	TCTGGGCTGGGGGGCTTGGGGCTTGGGGCTTGGGGCTTGGGG	480	421
Db	481	CCTCATCCACAATCCGGTATCACTCTCTGGGGGGGGGGGGGG	540	481	CCTCATCCACAATCCGGTATCACTCTCTGGGGGGGGGGGGGG	540	481
Qy	481	GG	540	481	GG	540	481
Db	541	GCTTCGGGGTGGACCATATGGTCCTTCTGTCGACATCTGCTG	600	541	GCTTCGGGGTGGACCATATGGTCCTTCTGTCGACATCTGCTG	600	541
Qy	541	GCTTCGGGGTGGACCATATGGTCCTTCTGTCGACATCTGCTG	600	541	GCTTCGGGGTGGACCATATGGTCCTTCTGTCGACATCTGCTG	600	541
Db	601	GCGATGGGGCCCTTGGGGCGGGGGGGGGGGGGGGGGGGGG	660	601	GCGATGGGGCCCTTGGGGCGGGGGGGGGGGGGGGGGGGGG	660	601
Qy	601	GGGGATGGGGCCCTTGGGGCGGGGGGGGGGGGGGGGGGGGG	660	601	GGGGATGGGGCCCTTGGGGCGGGGGGGGGGGGGGGGGGGGG	660	601
Db	661	TGACTCTAACGCTGAGCCGGCGCTGGGGGGGGGGGGGGGG	720	661	TGACTCTAACGCTGAGCCGGCGCTGGGGGGGGGGGGGGGG	720	661
Qy	661	TGACTCTAACGCTGAGCCGGCGCTGGGGGGGGGGGGGGGG	720	661	TGACTCTAACGCTGAGCCGGCGCTGGGGGGGGGGGGGGGG	720	661
Db	721	TGACACTAAGCTGGCTTAATGACTCTTGGGGGGGGGGGGGG	780	721	TGACACTAAGCTGGCTTAATGACTCTTGGGGGGGGGGGGGG	780	721
Qy	721	TGACACTAAGCTGGCTTAATGACTCTTGGGGGGGGGGGGGG	780	721	TGACACTAAGCTGGCTTAATGACTCTTGGGGGGGGGGGGGG	780	721
Db	781	TGGCGTCACTCTGTGAGGAGGGGGGGGGGGGGGGGGGGGG	840	781	TGGCGTCACTCTGTGAGGAGGGGGGGGGGGGGGGGGGGGG	840	781

QY 181 CTTACTACACCTGTGAGGCCCGGCTGCGCAACTCGGGGGCAC 240
 Db 181 CTTACTACACCTGTGAGGCCCGGCTGCGCAACTCGGGGGCAC 240
 QY 241 GCGCTTGATGCTGGCCGACCGGGCATGGAAAGTGGAGCTGGGG 300
 Db 241 GCGCTTGATGCTGGCCGACCGGGCATGGAAAGTGGAGCTGGGG 300
 QY 301 CGGGGGGGCGGGGGCTGGCTGGGGGGGGGGGGGGGGGGGGGG 360
 Db 301 CGGGGGGGCGGGGGCTGGCTGGGGGGGGGGGGGGGGGGGGGG 360
 QY 361 CGACCTCGCCAGGGAGTGGGAACTAAGGTCTGGCTGGGGGGGG 420
 Db 361 CGACCTCGCCAGGGAGTGGGAACTAAGGTCTGGCTGGGGGGGG 420
 QY 421 TCTGGCTTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 480
 Db 421 TCTGGCTTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 480
 QY 481 CCTCATCCAAATGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 540
 Db 481 CCTCATCCAAATGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 540
 QY 541 GCTTCGAGGTGAACTATGGGGGGGGGGGGGGGGGGGGGGGG 600
 Db 541 GCTTCGAGGTGAACTATGGGGGGGGGGGGGGGGGGGGGGGG 600
 QY 601 GCGATGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 660
 Db 601 GCGATGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 660
 QY 661 TGAATTCGAAACGCGCTGGGGGGGGGGGGGGGGGGGGGGGG 720
 Db 661 TGAATTCGAAACGCGCTGGGGGGGGGGGGGGGGGGGGGGGG 720
 QY 721 TGAACATAGCTGGCTATGTTGGGGGGGGGGGGGGGGGGGG 780
 Db 721 TGAACATAGCTGGCTATGTTGGGGGGGGGGGGGGGGGGGG 780
 QY 781 TGGCTCTCTCTCTATGGGGGGGGGGGGGGGGGGGGGGGGGG 840
 Db 781 TGGCTCTCTCTATGGGGGGGGGGGGGGGGGGGGGGGGGGGG 840
 QY 841 TGTCTCTCTCTCTATGGGGGGGGGGGGGGGGGGGGGGGGGG 900
 Db 841 TGTCTCTCTCTATGGGGGGGGGGGGGGGGGGGGGGGGGGGG 900
 QY 901 AGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 960
 Db 901 AGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 960
 QY 961 TGGGAGATACTTGGCAACTGGCATGGAGGGGGGGGGGGGGGG 1020
 Db 961 TGGGAGATACTTGGCAACTGGCATGGAGGGGGGGGGGGGGGG 1020
 QY 1021 GGCAGCCCATCGCTATGGGGGGGGGGGGGGGGGGGGGGGG 1080
 Db 1021 GGCAGCCCATCGCTATGGGGGGGGGGGGGGGGGGGGGGGG 1080
 QY 1081 TGGTGAACCCGATGAGGGGGGGGGGGGGGGGGGGGGGGGG 1140
 Db 1081 TGGTGAACCCGATGAGGGGGGGGGGGGGGGGGGGGGGGGG 1140
 QY 1141 CGCCGACCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 1200
 Db 1141 CGCCGACCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 1200
 QY 1201 TTGGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1260
 Db 1201 TTGGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1260

QY 1261 ACCTCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 1320
 Db 1261 ACCTCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 1320
 QY 1321 TGG 1380
 Db 1321 TGG 1380
 QY 1381 GACCCCAAGCTGGGGGGGGGGGGGGGGGGGGGGGGGGGG 1440
 Db 1381 GACCCCAAGCTGGGGGGGGGGGGGGGGGGGGGGGGGGGG 1440
 QY 1441 TCTCTCTGGAGTGGAACTGGGGGGGGGGGGGGGGGGGGGG 1500
 Db 1441 TCTCTCTGGAGTGGAACTGGGGGGGGGGGGGGGGGGGGGG 1500
 QY 1501 TCTGGAAATTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 1560
 Db 1501 TCTGGAAATTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 1560
 QY 1561 GAGCAAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 1620
 Db 1561 GAGCAAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 1620
 QY 1621 TCCCTTGCAACCGTCTAGCTGGGGGGGGGGGGGGGGGG 1680
 Db 1621 TCCCTTGCAACCGTCTAGCTGGGGGGGGGGGGGGGGGG 1680
 QY 1681 GCTCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 1740
 Db 1681 GCTCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 1740
 QY 1741 CTGAAACCAAGGGCTGGGGGGGGGGGGGGGGGGGGGGGG 1800
 Db 1741 CTGAAACCAAGGGCTGGGGGGGGGGGGGGGGGGGGGGGG 1800
 QY 1801 CAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 1860
 Db 1801 CAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 1860
 QY 1861 ATGCAAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 1920
 Db 1861 ATGCAAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 1920
 QY 1921 AAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAA 1939
 Db 1921 AAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAA 1939

RESULT 5
 ABX92437
 ID ABX92437 standard; cDNA; 1939 BP.
 XX
 AC ABX92437;
 XX
 DT 08-MAY-2003 (first entry)
 DB cDNA encoding human PRO853 polypeptide.
 XX
 XX Human; PRO polypeptide; secreted and transmembrane protein;
 XX immune disorder; diabetes; hyper-insulinemia;
 XX cardiac insufficiency; nervous system disorder; kidney disorder;
 XX bone disorder; cartilage disorder; arthritis; tumour; wound healing;
 XX genetic disorder; cytoskeletal; anti-tumour; antiinflammatory;
 XX antiarthritic; anti-tumour; vulnerability; antianaemic; dermatological;
 XX cardiac; gene, ss.
 OS Homo sapiens.

Qy	1646	AGTTAATTTCGCCATGTRATGAGGCGATAGGCTCCGAGCTAAGGAGCTGCC	PT	diagnosing, treating and/or preventing autoimmune, inflammatory, cell
Qy	1574	AGTTAATTACCCCATGTATGAGCGATAAGGCTCCGAGCTAAGGAGCTGCC	PT	proliferative, developmental, endocrine, eye, metabolic, and
Qy	1706	AGGGCTCACTGAGTAGGAGGAGGCTCTGGATCTAACCAAGGGTGAGCCAGG	PT	gastrointestinal disorders
Db	1634	AGGFTGCACTGAGTAGGAGGAGGCTCTGGATCTAACCAAGGGTGAGCCAGG	XX	Claim 5; Page 160, 1339B, English.
Db	1766	GCGGACTGCGCTAAGAGTGGGCTGAGAAGTGAGTCAGGCAGGGAGCTGAGG	CC	The present sequence is human drug metabolising enzyme (DME-3) cDNA.
Qy	1766	GCGGACTGCGCTAAGAGTGGGCTGAGAAGTGAGTCAGGCAGGGAGCTGAGG	CC	Human DME and its nucleic acid molecule are useful for the diagnosis, treatment and prevention of disorders associated with increased or decreased expression of DME. Examples of such disorders include, autoimmune/inflammatory disorder such as acquired immune deficiency
Db	1694	GCGGACTGCGCTAAGAGTGGGCTGAGAAGTGAGTCAGGCAGGGAGCTGAGG	CC	syndrome (AIDS), rheumatoid arthritis, osteoporosis, cell proliferative disorder such as actinic keratosis, atherosclerosis, developmental disorder such as epilepsy, anaemia, endocrine disorder such as acromegaly, creatinism, thyrotoxicosis; pancreatic disorder such as diabetes mellitus, eye disorder such as conjunctivitis, glaucoma, iritis; metabolic disorder such as Addison's disease, obesity, gastrintestinal disorder such as anorexia, dysphagia and hepatic tumours including nodular hyperplasia, adenomas and carcinomas. DME DNA is useful for creating 'knockin' humanised animals (pigs) or transgenic animals (mice or rats) to model human disease. DME DNA is also in useful is gene therapy. DME and its immunogenic fragment are useful for screening libraries of compounds in several drug screening assays.
Db	1826	TGCCCCATGGAGTAGGAGGAGGCTCCGGCGATCGAGGGCTGGGAGCTATGAGG	CC	XX
Qy	1826	TGCCCCATGGAGTAGGAGGAGGCTCCGGCGATCGAGGGCTGGGAGCTATGAGG	CC	1693
Db	1754	TGCCCCATGGAGTAGGAGGAGGCTCCGGCGATCGAGGGCTGGGAGCTATGAGG	CC	1825
Qy	1886	TTAAGCCCCCTGGGATAAACGGGTTGACCGCCAAAAAaaaaaaaaaaaaaaa	CC	1753
Db	1814	TTAAGCCCCCTGGGATAAACGGGTTGACCGCCAAAAAaaaaaaaaaaaaaaa	CC	1867
RESULT 7				
ID	AAD9938	standard; cDNA; 1779 BP.		
XX				
AC				
XX				
DT	12-SEP-2001 (first entry)			
XX				
DB				
		Human drug metabolising enzyme (DME-3) cDNA.		
XX				
KW		Human; drug metabolising enzyme; DME-3; immunosuppressive; gene therapy; cytotoxic; autoimmune disorder; inflammatory disorder; atherosclerosis; osteoporosis; eye disorder; hepatic tumour; Addison's disease; creatinism; rheumatoid arthritis; acquired immune deficiency syndrome; AIDS; anaemia; developmental disorder; endocrine disorder; iritis; aromegaly; epilepsy; thyrotoxicosis; pancreatic disorder; nodular hyperplasia; conjunctivitis; glaucoma; gastrointestinal disorder; nodular hyperplasia; conjunctivitis; glaucoma; actinic keratosis; metabolic disorder; dysphagia; anorexia; carcinoma; cell proliferative disorder; ss.		
XX				
OS		Homo sapiens.		
XX				
KEY		Location/Qualifiers		
PT		CDS		
PT		/*tag= a		
PT		/product= "Human drug metabolising enzyme (DME-3)"		
PT		sig_peptide		
PT		252..455		
PT		/*tag= b		
PT		455..1109		
PT		mat_peptide		
PT		/*tag= c		
PT		/product= "Mature drug metabolising enzyme (DME-3)"		
XX		W0200151638-A2.		
XX				
PD		19-JUL-2001.		
XX				
PP		12-JAN-2001; 2001WO-US01174.		
XX				
PR		14-JAN-2000; 2000US-0176139.		
PR		28-JAN-2000; 2000US-0177443.		
PR		28-JAN-2000; 2000US-0178574.		
PA		(INCYT) INCYTE GENOMICS INC.		
XX				
PI		Yang J., Baughn MR., Burford N., Au-Yong J., Lu DAM, Reddy R, Ring HZ, Hillman JR., Yee H., Azimzai Y., Yao MJ., Gandhi AR, Nguyen DB, Tang YT, Lal P., Bandhan O;		
XX				
DR		WPI, 2001-425874/45.		
XX				
PT		P-REDB; WAB05172.		
PT		Drug metabolizing enzymes and encoding polynucleotides, useful for		
Qy	731	CTGGCTTAATCTACTTTCGCCGGAGCTGCCAACAGCTTGCGCACTGGCGCACC	Qy	911 GCGCAGAACCCCTGATGCTCTACAGAGGCGATAGGCCCTCACTGGAGGAT
Db	582	CTGGCTTAATCTACTTTCGCCGGAGCTGCCAACAGCTTGCGCACTGGCGCACC	Db	762 GCGCAGAACCCCTGATGCTCTACAGAGGCGATAGGCCCTCACTGGAGGAT
Qy	791	TGCTATGAGGCCAACAGGGCTCTGAGCTGGAGCTGGCTGGCTGGCTGGCTGG	Qy	910 TGGCTGGCCACTTTGCGCCATGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG
Db	642	TGCTATGAGGCCAACAGGGCTCTGAGCTGGAGCTGGCTGGCTGGCTGGCTGG	Db	970 911 GCGCAGAACCCCTGATGCTCTACAGAGGCGATAGGCCCTCACTGGAGGAT
Qy	851	TGGCTGGCCACTTTGCGCCATGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG	Qy	821 912 TGGCTGGCCACTTTGCGCCATGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG
Db	702	TGGCTGGCCACTTTGCGCCATGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG	Db	822 TGGCTGGCCACTTTGCGCCATGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG

Db	353	ACCCAGCCTCAGAGCTCACCGATTTGCTPAGATACACCCAGBATTAGGCTAAG 412	PR	11-JUN-1999; 99US-0138625.
Qy	1236	TGAGCTGAGTCAGCTCTAACCTAACCTAGGCKAKAGTCGCTGAGCAGTCAT 1295	XX	
Db	413	TGAGCTGAGTCAGCTCTAACCTAACCTAGGCKAKAGTCGCTGAGCAGTCAT 472	PA	(HUMA-) HUMAN GENOME SCI INC.
Qy	1296	GTCTCTGAAACCTCGATGTTGAGGCAATGCCCTGAGCTGAC3GTTGAT 1355	XX	
Db	473	GTCTCTGAAACCTCGATGTTGAGGCAATGCCCTGAGCTGAC3GTTGAT 532	PI	Rosen CA, Ruben SM, Komatsoulis GA;
Qy	1356	CTGACTCTCGGGTACTCTGGGCCCCAGCTGCGTGCAGACTGACGGTTGT 1415	XX	
Db	533	CTGACTCTCGGGTACTCTGGGCCCCAGCTGCGTGCAGACTGACGGTTGT 592	DR	WPI: 2001-071148/08.
Qy	1416	GTGAGGAGATAATGGGATAATTCTCTGAGAGTACAGTAACCCGATGGAG 1475	XX	
Db	593	GTGAGGAGATAATGGGATAATTCTCTGAGAGTACAGTAACCCGATGGAG 652	PT	Nucleic acids encoding 47 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. cancers, Parkinson's disease and diabetic retinopathy -
Qy	1476	ATAGGGTATGCTAGACCTGCTCTGGAAATTGAGTAGTATTCTAGGCCC 1535	XX	
Db	653	ATAGGGTATGCTAGACCTGCTCTGGAAATTGAGTAGTATTCTAGGCCC 712	PT	
Qy	1536	CCCTATGATCTGATGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 1595	XX	
Db	713	CCCTATGATCTGATGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 772	CC	
Qy	1596	CCACATGAGATAGTGAATGATGCCCTTGCAACCTCTAGCTAGGTTAA 1655	CC	
Db	773	CCACATGAGATAGTGAATGATGCCCTTGCAACCTCTAGCTAGGTTAA 832	CC	
Qy	1656	CCCCATGTTAATGAGGGAAATTCTGGAGCTAAGCTGGCTTAC 1715	CC	
Db	833	CCCCATGTTAATGAGGGAAATTCTGGAGCTAAGCTGGCTTAC 892	CC	
Qy	1716	ATGAGTAGGAGGAGGAGCTGGATCTGGGAGGGAGCTGGATCTGGGAGCTG 1775	CC	
Db	893	ATGAGTAGGAGGAGGAGCTGGATCTGGGAGGGAGCTGGATCTGGGAGCTG 952	CC	
Qy	1776	GTAGATGGCTGAGAGTGAGTCTGGGAGGGAGCTGGATCTGGGAGCTG 1835	CC	
Db	953	GTAGATGGCTGAGAGTGAGTCTGGGAGGGAGCTGGATCTGGGAGCTG 1012	CC	
Qy	1836	GAGTAGGGAGCCTCTGGGAGGGAGCTGGGATCTGGGAGCTGGGAGCTG 1895	CC	
Db	1013	GAGTAGGGAGCCTCTGGGAGGGAGCTGGGAGCTGGGAGCTGGGAGCTG 1072	CC	
Qy	1896	CGGATTAAGCGCTGACGCC 1918	CC	
Db	1073	CGGATTAAGCGCTGACGCC 1095	CC	
<hr/>				
RESULT 9			Sequence 1140 BP; 269 A; 297 C; 330 G; 244 T; 0 other;	
AAFP26578			Query Match 36.0%; Score 698; DB 22; Length 1140;	
ID	AAFP26578	Best Local Similarity 99.5%; Pred. No. 7.3e-262; Matches 1088; Conservative 0; Mismatches 3; Indels 2; Gaps 2;		
XX		Query 827 CTGTCCTGCCTCACTTCTGGATGCTGGCCCTTTCGGCCCATGACTGCTG 886		
AC	AAFP26578;	Db 13 CTGTCCTGCCTCACTTCTGGATGCTGGCCCTTTCGGCCATGCTGCTG 72		
DT	27-MAR-2001 (first entry)	Qy 887 GTGCTGGGACCAAGAGGGGTGCGAGCACCCCTGATGTCCTCAAGGGC 946		
XX		Db 73 GTGCTGGGACCAAGAGGGGTGCGAGCACCCCTGATGTCCTCAAGGGC 132		
DR		Qy 947 ATGACCCCTCAGGGAGTATTCTGCACTGCTGAGCTGATGCTCTCAAGGT 1006		
Qy		Db 133 ATGACCCCTCAGGGAGTATTCTGCACTGCTGAGCTGATGCTCTCAAGGT 192		
Db		Qy 1007 GCGGAGACGGCGAGCCATCGCTATGGGGCCAGGAGGGCTGGAGGCT 1066		
Qy		Db 193 GCGGAGACGGCGAGCCATCGCTATGGGGCCAGGAGGGCTGGAGGCT 252		
Db		Qy 1067 GGCCTGGGAGGAGCTGAGCCGATGAAACCCAGCTGAGACTCGAGGCCA 1126		
Db		Db 253 GGCCTGGGAGGAGCTGAGCCGATGAAACCCAGCTGAGGCCA 312		
Qy		Qy 1127 TCTCTCTAGACCCACCTGGGACCCACCTGGGACCCACCTGGGACCC 1186		
Db		Db 313 TCTCTCTAGACCCACCTGGGACCCACCTGGGACCCACCTGGGACCC 372		
XX		Qy 1187 CAGAGCTCAGAGTTGCTAGATGAGCCAGGATCTGGCTAAGTGAGCTGAG 1246		
XX		Db 373 CAGAGCTCAGAGTTGCTAGATGAGCCAGGATCTGGCTAAGTGAGCTGAG 432		
DR		Qy 1247 ATCCGCTCTAACCTAGGGAGGAGCTGAGCTGAGCTGAGCTGAGCTGAG 1306		
DR		Db 433 ATCCGCTCTAACCTAGGGAGGAGCTGAGCTGAGCTGAGCTGAGCTGAG 492		
DR		Qy 1307 ACCTCGATGTTGAGGCACTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 1366		
OS		Db 493 ACCTCGATGTTGAGGCACTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 551		
XX		Qy 1367 TGGTACTCTGGAGGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 1425		
XX		Db 552 TGGTACTCTGGAGGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 611		
PP	01-JUN-2000; 2000WO-US15137.	Qy 1426 TATGGTATTTCTCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 1485		
XX				

QY	1486 GCTGAGACACTGTGCTCTCGGAAATTGGAGTGGATTTCAGGCCCCACCTTATTGA	1545	PI	Shimkets R.R., Leach M.
Db	672 GCTGAGACACTGTGCTCTCGGAAATTGGAGTGGATTTCAGGCCCCACCTTATTGA	731	XX	
Db	1546 TTCTCATGAGCTCTGAGGRGAGGAGGGTTCAGTGATGCACTGCCAACATGA	1605	DR	WPI; 2000-602362/57.
QY	732 TTCTCATGAGCTCTGAGGRGAGGAGGGTTCAGTGATGCACTGCCAACATGA	791	XX	P-PSDB; AAB42188.
Db	1606 GAATTTAGTGAACGTTGCTCCCTTGACCGCTAGCTAGTAACTACCCAGTT	1665	PT	Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease
QY	1666 AATGAGAGGGAATTGGCTCCGAGCTAAGGGACTCGCTAGGGACTGAGTAC	1725	XX	
Db	792 GAATTTAGTGAACGTTGCTCCCTTGACCGCTAGCTAGTAACTACCCAGTT	851	XX	
QY	852 AATGAGAGGGAATTGGCTCCGAGCTAAGGGACTGAGTAC	911	XX	
Db	1726 AGGAGGGCTGGATCTGACCCAGGGCTGGCCCTGGCCTCTGGTAAAGATGG	1785	XX	
QY	912 AGGAGGGCTGGATCTGACCCAGGGCTGGCCCTGGCCTCTGGTAAAGATGG	971	XX	
Db	1786 TCGCTGAGAAGTGTGACTTGGCCAGGGCAGCTGGTATGAGGTAGGG	1845	CC	AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORF X open reading frames 1 to 316. The ORF X sequences have activities such as: cytostatic; hepatotropic; vulnerability; antipsoratic; antiparkinsonian; nootropic; neuroprotective; osteoprotective; anticonvulsant; antiarthritic; immunosuppressive; immunostimulant; cardiotropic; thrombolytic; coagulant; vasotropism; antidiabetic; hypotensive; dermatological; antiviral; immunosuppressive; antiinflammatory; antibacterial; antiviral; antithyroid; and antianemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORF X-associated disorder. The nucleic acids can be used to express ORF X protein in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anemia, burns, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease, to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
Db	972 TCGCTGAGAAGTGTGACTTGGCCAGGGCTGGCCCTGGCCTCTGGTAAAG	1031	CC	
QY	1846 ACGCTTCCGGCGATGCGAGGGCTGGGCATCTGTAATCTGAGACCCCTCGGAAATAAG	1905	CC	
Db	1032 ACGCTTCCGGCGATGCGAGGGCTGGGCATCTGTAATCTGAGACCCCTCGGAAATAAG	1091	CC	
QY	1906 CGCGTGTACGCC 1918		CC	
Db	1092 CGCGTGTACGCC 1104		CC	
RESULT	11		XX	
ID	AAC76397 Standard; cDNA; 598 BP.		XX	
XX			XX	
AC	AAC76397;		XX	
XX	08-FEB-2001 (first entry)		XX	
DB	Human ORF X poly nucleotide sequence SEQ ID NO:3903.		XX	
XX			XX	
QY	Human, open reading frame; ORF X; detection; cytostatic; hepatotropic; vulneratory; antipsoratic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteoprototic; antiarthritic; immunosuppressive; cardiotropic; immunostimulant; thrombolytic; coagulant; vasotropism; hypotensive; dermatological; immunosuppressive; antinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antidiabetic; antidiabetic; antihypertensive; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation; thrombosis; contraceptive; SB; Homo sapiens.		XX	
PN	W020058473-A2.		XX	
PD	05-OCT-2000.		XX	
PR	31-MAR-2000; 2000WO-US08621.		XX	
PR	02-APR-1999; 99US-0127607.		XX	
PR	05-APR-1999; 99US-0127636.		XX	
PR	30-MAR-2000; 2000US-0540763.		XX	
PA	(CURA-) CURAGEN CORP.		XX	
RESULT	12		XX	
AA166494			XX	
ID	AA166494 Standard; cDNA; 397 BP.		XX	
AC	AA166494.		XX	

XX DT 09-APR-2001 (first entry)
 XX DT Novel human polynucleotide, SEQ ID NO: 2250.
 XX ID AAT19666 standard; cDNA to mRNA; 186 BP.
 XX AC AAT19666;
 XX DT 28-JUN-1996 (first entry)
 XX DB Human gene signature HUMGS00736.
 XX Gene signature; messenger RNA; mRNA; relative abundance; frequency;
 XX human; cloning; mapping; non-biased library; diagnosis; detection;
 XX cell typing; abnormal cell function; ss;
 XX OS Homo sapiens.
 XX PN WO200102568-A2.
 XX PD 11-JAN-2001.
 XX PP 30-JUN-2000; 2000WO-US18374.
 XX PR 02-JUL-1999; 99PCT-0142310.
 XX PR 02-JUL-1999; 99US-0142311.
 XX PA (CHIR) CHIRON CORP.
 XX PA (HISEB) HISEQ INC.
 XX PI Williams LT, Escobedo J, Innis MA, Garcia PD, Klinger J, Kasean A;
 PI Reinhard C, Randazzo P, Kennedy GC, Pot D, Jamison G, Dumanic R;
 PI Crenjaku R, Dumanic S, Dickson M, Lapat I, Leibkowitz D;
 PI Kita D, Garcia V, Jones LW, Strache-Crain B;
 DR WPI, 2001-091805/10.
 XX PT Library of polynucleotides for diagnosing a cancerous state of a
 PT mammalian cell and detecting cancer, particularly of the colon or
 PT prostate, comprises 3351 human polynucleotide sequences -
 XX PS Claim 9; Page 873; 1046pp; English.
 XX CC The present sequence is one of 3351 sequences in a library of human
 CC polynucleotides. The library is used to detect differentially expressed
 CC genes correlated with a cancerous state of a mammalian cell and can
 CC detect colon, prostate, breast and lung cancer. The library can be used
 CC to produce probes for detection of mRNA and to produce additional copies
 CC of the polynucleotides. The probes can be used for chromosome mapping of
 CC the polynucleotide and for detection of transcription levels. Ribozymes
 CC or antisense oligonucleotides can be generated. The polynucleotides and
 CC their gene products are used as genetic or biochemical markers (e.g. in
 CC blood or tissues) that will detect the earliest changes along the
 CC carcinogenesis pathway and/or monitor the efficacy of therapies and
 CC preventive interventions. The polynucleotides, polypeptides and
 CC antibodies against them can be used in pharmaceutical compositions to
 CC treat the cancers and proliferative disorders such as neoplasia,
 CC dysplasia and hyperplasia.
 XX SQ Sequence 397 BP; 74 A; 125 G; 82 T; 0 other;
 Query Match 10.3%; Score 200; DB 22; Length 397;
 Best Local Similarity 100.0%; Pred. No. 3.7e-68;
 Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 716 TATGTGACACTAACCTGGCTAATGTTACTGTTGCCGAGCTGCGCCACCGCGCTGG 775
 Db 31 TATGTGACACTAACCTGGCTAATGTTACTGTTGCCGAGCTGCGCCACCGCGCTGG 90
 QY 776 GGCCTGGCTCACCTGCTATGCCGACCCAGGGCTTGACTCGAGCTGCTCTGG 835
 Db 91 GGCCTGGCTCACCTGCTATGCCGACCCAGGGCTTGACTCGAGCTGCTCTGG 150
 QY 836 CGCGATGTTCTGGATGGCTGGCCACTTTGGCCATTTGGTTGGCTGGCTGG 895
 Db 151 CGCCATGTTCTGGATGGCTGGCCACTTTGGCCATTTGGCTGGCTGGCTGG 210
 QY 896 GCACCAAGGGGGGCCA 915
 Db 211 GCACCAAGGGGGGCCA 230

RESULT 13
 XX DT AAT19666 standard; cDNA to mRNA; 186 BP.
 XX ID AAT19666
 XX AC AAT19666;
 XX DT 01-JUN-1995.
 XX PR 12-NOV-1993; 93JP-0355504.
 XX PA (MATS/) MATSUBARA K.
 XX PA (OKUB/) OKUBO K.
 XX PI Matsubara K, Okubo K.
 DR WPI, 1995-206931/27.
 XX PT Identifying gene signatures in 3'-directed human cDNA library - e.g.
 PT for diagnosis of abnormal cell function, by preparing cDNA that
 PT reflects relative abundance of corresp. mRNA in specific human
 PT tissues
 XX PS Claim 1; Page 445; 2245pp; Japanese.
 XX CC A single-stranded DNA (or its complementary strand or the corresp.
 CC double-stranded DNA) which comprises one of the "7837 "GS" sequences
 CC given in AAT19001-T26337 and which is able to hybridise to part of
 CC human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)
 CC sequences were obtained from 3'-directed cDNA library prepared
 CC from various human tissues; synthesis of cDNA was initiated from the
 CC 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-
 CC untranslated sequence is unique to a particular mRNA species, almost
 CC all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library
 CC is constructed so as to reflect accurately the relative abundance of
 CC different mRNA in the particular tissue from which it was derived.
 CC The appearance frequency of a given GS in a cDNA library can be
 CC determined (esp. using primers and probes derived from the GS
 CC sequences) as a means of diagnosing abnormal cell function or for
 CC recognising different cell types.
 XX SQ Sequence 186 BP; 42 A; 42 C; 67 G; 31 T; 4 other;
 Query Match 4.7%; Score 92; DB 16; Length 186;
 Best Local Similarity 100.0%; Pred. No. 4.1e-56;
 Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 174 AACCCAAAGGTCAGGCCAGGGCTTGCTTAAGTGGGGCTAGAACGAGTCAG 1803
 Db 8 AACCCAAAGGTCAGGCCAGGGCTTGCTTAAGTGGGGCTAGAACGAGTCAG 67
 QY 1804 GGCAGGGCACTGGTACAGGCGCCATGG 1835
 Db 68 GGCAGGGCACTGGTACAGGCGCCATGG 99

RESULT 14
 ABK64203/C
 ID ABK64203 standard; DNA; 175 BP.

XX
 DT 09-APR-2001 (first entry)
 DB Novel human polynucleotide, SEQ ID NO: 2250.
 XX
 KW Human; cyrostatic; gene therapy; colon cancer; prostate cancer;
 KW breast cancer; lung cancer; cancer detection; ss.
 OS Homo sapiens.
 XX
 PN WO20102568-A2.
 XX
 PD 11-JAN-2001.
 XX
 PP 30-JUN-2000; 2000WO-US18374.
 XX
 PR 02-JUL-1999; 99US-0142310.
 XX
 PR 02-JUL-1999; 99US-0142311.
 XX
 PA (CHIR) CHIRON CORP.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Williams LT, Escobedo J, Tunis MA, Garcia PD, Klinger J, Kassam A;
 PI Crkencakov R, Drmanac R, Labat I, Leshkowitz D;
 PI Kita D, Garcia V, Jones LW, Strachan-Brain B;
 DR WPI, 2001-091805/10.
 XX
 PT Library of polynucleotides for diagnosing a cancerous state of a
 PT mammalian cell and detecting cancer, particularly of the colon or
 PT prostate, comprises 3351 human polynucleotide sequences -
 XX
 P9 Claim 9, Page 873; 1046pp; English.
 CC The present sequence is one of 3351 sequences in a library of human
 CC polynucleotides. The library is used to detect differentially expressed
 CC genes correlated with a cancerous state of a mammalian cell and can
 CC detect colon, prostate, breast and lung cancer. The library can be used
 CC to produce probes for detection of mRNA and to produce additional copies
 CC of the polynucleotides. The probes can be used for chromosome mapping of
 CC the polynucleotide and for detection of transcription levels. Ribosomes and
 CC or antisense oligonucleotides can be generated. The polynucleotides and
 CC their gene products are used as genetic or biochemical markers (e.g. in
 CC blood or tissues) that will detect the earliest changes along the
 CC carcinogenesis pathway and/or monitor the efficacy of therapies and
 CC preventive interventions. The polynucleotides, polypeptides and
 CC antibiotics against them can be used in pharmaceutical compositions to
 CC treat the cancers and proliferative disorders such as neoplasia,
 CC dysplasia and hyperplasia.
 XX
 Sequence 397 BP; 74 A; 116 C; 125 G; 82 T; 0 other;
 Query Match 10.3%; Score 200; DB 22; Length 397;
 Best Local Similarity 100.0%; Pred. No. 3.7e-08;
 Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 716 TATCTGACACTAGCTGCGCTAATGATCTGTTGCCCGAGGCTCGCAACCGAGTGTAG 775
 Db 31 TATCTGACACTAGCTGCGCTAATGATCTGTTGCCCGAGGCTCGCAACCGAGTGTAG 90
 Qy 776 GCACTGGGGCTGCGCTGATGAGCCACCGGGCTGAGCTGGAGCTGCTG 835
 Db 91 GCGCTGGGGCTGAGCTGGCTGAGCCACCGGGCTGAGCTGGCTG 150
 Qy 836 CSGCATGTTCTGATGCGCTGAGCTGGCTGAGCTGGCTGAGCTGGCTGAGCTGGCTG 895
 Db 151 CGCGATGTTCTGATGCGCTGAGCTGGCTGAGCTGGCTGAGCTGGCTGAGCTGGCTG 210
 Qy 896 GCGCAGGAGGGGGTGCAGA 915
 Db 211 GCGCAGGAGGGGGTGCAGA 230

RESULT 13
 AAT19666
 ID AAT19666 standard, cDNA to mRNA, 186 BP.
 XX
 KW Human gene signature HUMGS00733.
 KW Gene signature; messenger RNA; mRNA; relative abundance; frequency;
 KW human; cloning; mapping; non-biased library; diagnosis; detection;
 KW cell typing; abnormal cell function; ss.
 OS Homo sapiens.
 XX
 PN WO9514772-A1.
 XX
 PR 11-NOV-1994; 94WO-JP01916.
 XX
 PR 12-NOV-1993; 93JP-0355504.
 XX
 PA (MATS/) MATSUBARA K.
 PA (OKUB/) OKUBO K.
 XX
 PI Matsubara K, Okubo K;
 XX
 DR WPI, 1995-206931/27.
 XX
 PT Identifying gene signatures in 3'-directed human cDNA library - e.g.
 PT for diagnosis of abnormal cell function, by preparing cDNA that
 PT reflects relative abundance of corresp. mRNA in specific human
 PT tissues
 XX
 PS Claim 1, Page 445; 2245pp; Japanese.
 CC A single-stranded DNA (or its complementary strand or the correponding
 CC double-stranded DNA) which comprises one of the 7837 "GS" sequences
 CC given in AAT19001-T26837 and which is able to hybridise to part of
 CC human genomic DNA, cDNA or mRNA is claimed. (The GS (Gene Signature)
 CC sequences were obtained from 3'-directed cDNA libraries prepared
 CC from various human tissues. Synthesis of cDNA was initiated from the
 CC 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-
 CC untranslated sequence is unique to a particular mRNA species, almost
 CC all the 3'-orientated cDNAs hybridise with specific mRNAs. Each library
 CC is constructed so as to reflect accurately the relative abundance of
 CC different mRNAs in the particular tissue from which it was derived.
 CC The appearance frequency of a given GS in a cDNA library can be
 CC determined (e.g. using primers and probes derived from the GS
 CC sequences) as a means of diagnosing abnormal cell function or for
 CC recognising different cell types.
 XX
 SQ Sequence 186 BP; 42 A; 42 C; 67 G; 31 T; 4 other;
 Query Match 4.7%; Score 92; DB 16; Length 186;
 Best Local Similarity 100.0%; Pred. No. 4.1e-26;
 Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1744 AACCGAGGGCTGAGCCACGGCCACCTGGCGTAAGATGGTGTGAGAGTGAGTCAG 1803
 Db 8 AACCGAGGGCTGAGCCACGGCCACCTGGCGTAAGATGGTGTGAGAGTGAGTCAG 67
 Qy 1804 GGCAGGGCACTGGTGTGAGGGTGCAG 1335
 Db 68 GGCAGGGCACTGGTGTGAGGGTGCAG 99

RESULT 14
 ABK64203-C
 ID ABK64203 standard; DNA; 175 BP.

AC	ABK64203;	XX	AA179552;
DT	18-JUN-2002 (first entry)	XX	AA179552;
DE	Human benign prostatic hyperplasia gene #98.	XX	AA179552;
XX	Human; benign prostatic hyperplasia; BPH; prostate cancer; gene; ds.	XX	AA179552;
KW	Homo sapiens.	XX	AA179552;
OS	W0200212440-A2.	XX	AA179552;
XX	14-FEB-2002.	XX	AA179552;
PD	14-FEB-2002.	XX	AA179552;
PP	07-AUG-2001; 2001WO-US24708.	XX	AA179552;
XX	07-AUG-2000; 2000US-223323P.	XX	AA179552;
PR	05-JUN-2001; 2001US-0873319.	XX	AA179552;
XX	(GENE-) GENE LOGIC INC.	XX	AA179552;
PA	(NIBB) JAPAN TOBACCO INC.	XX	AA179552;
XX	Munger WE, Kulkarni P, Getzenberg RH, Waga I, Yamamoto J;	XX	AA179552;
XX	WPI; 2002-257476/30.	XX	AA179552;
PT	Identifying drugs for and diagnosing benign prostatic hyperplasia, by detecting expression levels of one or more genes in prostate cells from patient that are differentially regulated compared to normal prostate cells -	XX	AA179552;
XX	Disclosure; Page 109; 444pp; English.	XX	AA179552;
CC	The invention relates to a method of diagnosing (I) the onset or progression of benign prostatic hyperplasia (BPH), or screening (II) for or identifying an agent that modulates the onset or progression of BPH. The method is based on changes in gene expression in BPH tissue isolated from patients exhibiting different clinical states of prostate hyperplasia as compared to normal prostate tissue. (I) comprises detecting the expression levels of one or more genes in prostate cells from the subject that are differentially regulated compared to normal prostate cells. (II) comprises preparing a first gene expression profile of BPH cells or BPH-like cell population, exposing the cells to the agent, preparing a second gene expression profile of the agent exposed cells, and comparing the first and second gene expression profiles.	XX	AA179552;
CC	(I) is useful for diagnosing the onset or progression of BPH. (II) is useful for identifying an agent that modulates the onset or progression of BPH. The methods are useful to present information identifying the expression level in a tissue or cells, by comparing the expression level of genes given in the specification in the tissue or cells to the expression levels of at least one gene in the tissue or cell sample compared to the expression level in BPH. Agents using (II) are useful for treating BPH or prostate cancer. ABK64106-ABK64160 represent human benign prostatic hyperplasia gene sequences of the invention.	XX	AA179552;
SQ	Sequence 175 BP; 27 A; 62 C; 37 G; 49 T; 0 other;	XX	AA179552;
Query Match	4.5%; Score 89; DB 24; Length 175;	XX	AA179552;
Best Local Similarity	100.0%; Pred. No. 1.5e-24;	XX	AA179552;
Matches	88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	XX	AA179552;
OY	1762 CAGGGCCGACTGGCGTAAGATGGTGTGAGAAGTGGAGCTGAGGCTAGGGCAGGTGTATC 1821	OY	594 GCTCTGAAAGCCATGCGCCCTAGCGCGCTGCTGGGGTACCTCGCTGCG 644
Db	175 CAGGGCCGACTGGCGTAAGATGGTGTGAGAAGTGGAGCTGAGGCTAGGGCAGGTGTATC 116	Db	1 GCTCTGAAAGCCATGCGCCCTAGCGCGCTGCTGGGGTACCTCGCTGCG 51
OY	1822 GAGGTGCCCCATGGGGAGTGGGGAGGC 1849	OY	594 GCTCTGAAAGCCATGCGCCCTAGCGCGCTGCTGGGGTACCTCGCTGCG 644
Db	115 GAGGTGCCCCATGGGGAGTGGGGAGGC 88	Db	1 GCTCTGAAAGCCATGCGCCCTAGCGCGCTGCTGGGGTACCTCGCTGCG 51
Search completed: January 31, 2004, 04:50:06	Job time : 557 secs		